

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 27, 2003, 20:11:16 ; Search time 5026 Seconds

(without alignments)
10752.411 Million cell updates/sec

Title: us-09-934-249-1

Perfect score: 1321

Sequence: 1 cgaccgcgcgtctcgagcgga.....ctgcgtagtgtaaaagcgag 1321

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 2888711 seqs, 20454813386 residues

Size: 8

Total number of hits satisfying chosen parameters: 4335150

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

GenEmbl:
1: gb_da:
2: gb_hcg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vi:
15: em_da:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mu:
20: em_om:
21: em_or:
22: em_ov:
23: em_pat:
24: em_ph:
25: em_pl:
26: em_ro:
27: em_sts:
28: em_un:
29: em_vi:
30: em_htg_hum:
31: em_htg_inv:
32: em_htg_other:
33: em_htg_mus:
34: em_htg_pln:
35: em_htg_rnd:
36: em_htg_mam:
37: em_htg_vtl:
38: em_sy:
39: em_htgo_hum:
40: em_htgo_mus:
41: em_htgo_other:

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1321	100.0	1321	6	AX392417 Sequence
2	1229	93.0	4839	6	AF305616 Homo sapi
3	861	65.2	861	6	AX392419 Sequence
4	838	63.4	1061	9	BC015918 Homo sapi
5	800	60.6	1141	9	AF224278 Homo sapi
6	800	60.6	1818	9	AY128643 Homo sapi
7	593	44.9	61505	9	AF305426 Homo sapi
8	593	42.4	130435	9	HS171817 Homo sapi
9	560	42.4	1583	6	AX593655 Human DNA
10	521	39.4	150224	6	HS0105917 Human DNA
11	401	30.4	408	6	AX071267 Sequence
12	302	22.9	693	6	AX392430 Sequence
13	271	20.5	812	6	AX011709 Sequence
14	51	3.9	51	6	AX199565 Sequence
15	44	3.3	651	10	AF220208 Mus muscu
16	44	3.3	878	6	AX392428 Sequence
17	44	3.3	1379	10	BC036995 Mus muscu
18	44	3.3	156698	10	AL837509 Mouse DNA
19	44	3.3	175754	2	AC110189 Mus muscu
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21	44	3.3	176821	2	AL837520 Mus muscu
22	42	3.2	673	6	AX525744 Sequence
23	42	3.2	249554	2	AC139417 Rattus no
24	42	3.2	258632	2	AC111878 Rattus no
25	41	3.1	475	6	AX392431 Sequence
26	41	3.1	175754	2	AC110189 Mus muscu
27	37	2.8	175363	2	AC116815 Mus muscu
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30	34	2.6	44312	2	AB065453 Homo sapi
31	34	2.6	110000	2	AC106698 Rattus no
32	34	2.6	112883	9	AC009404 Homo sapi
33	34	2.6	118959	8	OSTN00235 Oryza sat
34	34	2.6	153308	8	AC118668 Genomic s
35	34	2.6	198689	2	AC126463 Rattus no
36	34	2.6	19471	2	AC134632 Rattus no
37	34	2.6	221100	2	AC112841 Rattus no
38	34	2.6	233939	2	AC105853 Rattus no
39	34	2.6	237026	2	AC103439 Rattus no
40	34	2.6	237151	2	AC137424 Rattus no
41	34	2.6	242493	2	AC137322 Rattus no
42	34	2.6	247356	2	AC111257 Rattus no
43	34	2.6	266344	9	AC005158 Homo sapi
44	34	2.6	275229	2	AC098198 Rattus no
45	34	2.6	305075	2	AC106355 Rattus no

ALIGNMENTS

RESULT 1
LOCUS AX392417 1321 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 1 from Patent WO0216416.
ACCESSION AX392417
VERSION AX392417.1 GI:19700732
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Lee R.T., Landschulz, K.T., Kennedy, S.P., Thompson, J.F. and
Turi, T.G.
TITLE Diagnosis and treatment of cardiovascular conditions

Pred. No. is the number of results predicted by chance to have a


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Oy 613 GTCGACAGGTCCTTCATCAGCCGACAGCCAGGAGGAGAGAGAGATGCCCTGTC 672
Db 181 GTCTGACAGGTCCTTCATCAGCCGACAGCCAGGAGGAGAGAGATGCCCTGTC 240
Oy 673 CTCAGAGAGATGCTGTGAGCCCTGCGAGAGCAGATGTCTAGGACAGATGCCAGAGCC 732
Db 241 CTCAGAGAGATGCTGTGAGCCCTGCGAGAGCAGATGTCTAGGACAGATGCCAGAGCC 300
Oy 733 GCAGGTCTAGCCGCCGCTGAGCCACCAGCCGCTGAGCCGCTGAGCCGCTGAGCCG 792
Db 301 GCAGGTCTAGCCGCCGCTGAGCCACCAGCCGCTGAGCCGCTGAGCCGCTGAGCCG 360
Oy 793 GGAGGCTCTGAGCCGCCGCTGAGCCACCAGCCGCTGAGCCGCTGAGCCGCTGAGCCG 852
Db 361 GGAGGCTCTGAGCCGCCGCTGAGCCACCAGCCGCTGAGCCGCTGAGCCGCTGAGCCG 420
Oy 853 ACCGACCATCTGCTGTCTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 912
Db 421 GCCACCATCTGCTGTCTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Oy 913 CCAGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 972
Db 481 CCAGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Oy 973 AAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1032
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Db 601 CCCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
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JTL 5
 AF224278
 LOCUS AF224278 1141 bp mRNA linear PRI 18-JUL-2000
 DEFINITION Homo sapiens PMEPA1 protein (PMEPA1) mRNA, complete cds.
 ACCESSION AF224278
 VERSION AF224278.1 GI:9255808
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1141)
 Xu,L.L., Shanmugam,N., Segawa,T., Sesterhenn,I.A., McLeod,D.G.,
 Moul,J.W. and Srivastava,S.
 A novel androgen-regulated gene, PMEPA1, located on chromosome
 20q13 exhibits high level expression in prostate
 Genomics 66 (3), 257-263 (2000)
 JOURNAL MEDLINE
 PUBMED 10873380
 2 (bases 1 to 1141)
 Xu,L.L., Shanmugam,N., Segawa,T., Sesterhenn,I.A., McLeod,D.G.,
 Moul,J.W. and Srivastava,S.
 Direct Submission
 JOURNAL Submitted (12-JAN-2000) CPDR, USUHS, 1530 East Jefferson Street,

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FEATURES
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    /db_xref="taxon:9606"
    /chromosome="20"
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    /cell_line="LNCaP"
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    96..854
    /CDS
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    /note="type 1b transmembrane protein; expression is induced in response to the synthetic androgen, R1881; expression is abundant in, and restricted to, prostate glandular epithelial cells; similar to the predicted protein encoded by sequence deposited at Genbank Accession Number NP_004329"
    /codon_start=1
    /product="PMEPA1 protein"
    /protein_id="AAF86322.1"
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    Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    522 CGAGCTGAGAGTTTGTGATGATCATCATCATGCTGTGTGTATGATGATGATGATG 581
    Db 100 CGAGCTGAGAGTTTGTGATGATCATCATCATGCTGTGTGTATGATGATGATGATG 159
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    Db 160 TGATCAGTGCCTGTGTGAGCCACTACAGCTGTGTGACAGGTCCTTCATCAGCCGAGCA 219
    Oy 642 GCCAGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 701
    Db 220 GCCAGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 279
    Oy 702 GCACAGTGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 761
    Db 280 GCACAGTGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 339
    Oy 762 ACCGCTGTGCGCTGTGCGCCCTTGTGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAG 821
    Db 340 ACCGCTGTGCGCTGTGCGCCCTTGTGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 399
    Oy 822 ATCCGTACTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 881
    Db 400 ATCCGTACTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 459
    Oy 882 ACCCCGACCCCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 941
    Db 460 ACCCCGACCCCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 519
    Oy 942 AACTGACCGGAGAGTGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1001
    Db 520 AACTGACCGGAGAGTGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 579
    Oy 1002 TGGATAGTGCAGAGCTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1061
    Db 580 TGGATAGTGCAGAGCTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 639
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QY	DB	Query Match	Best Local Similarity	Matches	Score	DB	Length	Gaps
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522	CGAGAGTGGAGTTTGTTCAGATCATCATCATCTGCTGTGATGATGATGATGATGATGATG	60.6%	100.0%	800	800	Conservative	0	0

[illegible]

repeat_region 427..626
/note="4 copies 50 mer 71% conserved"
repeat_region 707..812
/note="53 copies 2 mer cc 61% conserved"
repeat_region 967..2752
/note="893 copies 2 mer gg 54% conserved"
repeat_region 982..2730
/note="33 copies 53 mer 54% conserved"
repeat_region 1177..1820
/note="4 copies 161 mer 64% conserved"
repeat_region 1204..1371
/note="3 copies 56 mer 75% conserved"
repeat_region 1358..2757
/note="28 copies 50 mer 54% conserved"
repeat_region 1675..2718
/note="18 copies 58 mer 55% conserved"
repeat_region 1843..2346
/note="9 copies 56 mer 64% conserved"
repeat_region 1852..2079
/note="4 copies 57 mer 86% conserved"
repeat_region 2028..2632
/note="11 copies 55 mer 60% conserved"
repeat_region 2087..2257
/note="3 copies 57 mer 83% conserved"
repeat_region 2228..2497
/note="5 copies 54 mer 75% conserved"
repeat_region 2583..2716
/note="2 copies 67 mer 82% conserved"
repeat_region 3378..3426
/note="1MB4 repeat: matches 6088..6136 of consensus"
repeat_region 3799..3896
/note="Charl1el repeat: matches 681..781 of consensus"
repeat_region 5331..5793
/note="MUT1B repeat: matches 14..466 of consensus"
repeat_region 5797..5988
/note="6 copies 32 mer 86% conserved"
repeat_region 5855..5978
/note="31 copies 4 mer gcac 61% conserved"
repeat_region 6474..6591
/note="MIR repeat: matches 91..218 of consensus"
repeat_region 6592..6723
/note="FLAM_C repeat: matches 1..132 of consensus"
repeat_region 6952..7021
/note="L2 repeat: matches 2637..2705 of consensus"
repeat_region 7358..7671
/note="Alusx repeat: matches 1..312 of consensus"
repeat_region 8521..8554
/note="Alu repeat: matches 1..34 of consensus"
repeat_region 8863..9217
/note="MUT1D repeat: matches 105..505 of consensus"
repeat_region 9228..9746
/note="L2 repeat: matches 1459..2028 of consensus"
repeat_region 9880..10089
/note="L2 repeat: matches 2292..2511 of consensus"
repeat_region 10094..10206
/note="AluB repeat: matches 188..300 of consensus"
repeat_region 10263..10573
/note="AluB repeat: matches 1..308 of consensus"
repeat_region 10658..10753
/note="L2 repeat: matches 2647..2749 of consensus"
repeat_region 11816..12380
/note="L1R1B repeat: matches 1..580 of consensus"
repeat_region 12519..12813
/note="L1R1C repeat: matches 257..386 of consensus"
repeat_region 13559..13726
/note="L1M2 repeat: matches 6032..6331 of consensus"
repeat_region 13585..13716
/note="3 copies 56 mer 73% conserved"
repeat_region 13586..13717
/note="22 copies 6 mer ctctct 67% conserved"
repeat_region 13588..13715
/note="66 copies 2 mer tc 68% conserved"
repeat_region 13589..13724
/note="4 copies 32 mer 78% conserved"

misc_feature /note="34 copies 4 mer ctlt 77% conserved"
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14313..14437 /note="match: GSS: Em: A0592603"
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repeat_region 15021..15110 /note="3 copies 32 mer 79% conserved"
repeat_region 15026..15109 /note="45 copies 2 mer ac 80% conserved"
repeat_region 15028..15111 /note="7 copies 12 mer 82% conserved"
repeat_region 15029..15108 /note="14 copies 6 mer cacaca 82% conserved"
repeat_region 15273..15399 /note="20 copies 4 mer acac 83% conserved"
repeat_region 15420..15721 /note="L2 repeat: matches 2159..2285 of consensus"
repeat_region 16333..16396 /note="Alusx repeat: matches 1..303 of consensus"
repeat_region 16575..16690 /note="2 copies 32 mer 98% conserved"
repeat_region 18049..18168 /note="L2 repeat: matches 2596..2711 of consensus"
repeat_region 18312..18438 /note="MIR repeat: matches 86..211 of consensus"
repeat_region 18585..18776 /note="MIR repeat: matches 138..250 of consensus"
repeat_region 19211..19290 /note="MER20 repeat: matches 7..217 of consensus"
repeat_region 20413..20463 /note="MIR repeat: matches 72..154 of consensus"
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/note="match: GSS: Em: A0136459"
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repeat_region 23577..23646 /note="2 copies 35 mer 100% conserved"
repeat_region 24257..24591 /note="L2 repeat: matches 2336..2710 of consensus"
repeat_region 25580..25611 /note="L2 repeat: matches 2336..2710 of consensus"
repeat_region 26333..26643 /note="16 copies 2 mer tc 87% conserved"
repeat_region 27603..27684 /note="AluY repeat: matches 1..310 of consensus"
repeat_region 27823..28041 /note="L2 repeat: matches 2661..2739 of consensus"
repeat_region 28129..28259 /note="MIR repeat: matches 38..242 of consensus"
repeat_region 31203..31356 /note="FLAM_C repeat: matches 1..127 of consensus"
repeat_region 32224..32522 /note="L1M5 repeat: matches 6015..6176 of consensus"
/note="Alusx repeat: matches 1..298 of consensus"

Query Match 44.9%; Score 593; DB 9; Length 130435;
Best Local Similarity 100.0%; Pred. No. 1e-294;
Matches 593; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 128443 AGCCGAGCTACGCCCGCTGCGCCACGACCGCTGCGCCCTTGCC 128384
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QY 789 AGCGGAGGCTTCACCGCTTCACCGCCACCTATCCGATCGACGAGATGACC 848
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DB 128383 AGCGGAGGCTTCACCGCTTCACCGCCACCTATCCGATCGACGAGATGACC 128324

OY	849	GGCCACCCACCATCTCCTGGCTGTAGACGGGGAGAGAGCCCCACCCTTCACAGGGCCCTTGA	908
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Db	1282653	CCCTTCACAGCTTCGGGAGACCCCGAGCAGCAGCTTGAATCGAACCGGAGTGGTTCGGCGAC	1282044
OY	969	CCCCAACAGAACCATCTTTCGACAGTGAACCTGATGATAGTGTGCGAGGCTTGGCGGCCCT	1028
Db	1282033	CCCCAACAGAACCATCTTTCGACAGTGAACCTGATGATAGTGTGCGAGGCTTGGCGGCCCT	1281444
OY	1029	GGCCCCCAGCAGTAACTCCTGGGATCAGAGCCAGCGATGCTACGGCAGACGGCGGGCGCATGG	1088
Db	128143	GGCCCCCAGCAGTAACTCCTGGGATCAGAGCCAGCGATGCTACGGCAGACGGCGGGCGCATGG	1280844
OY	1089	AGGGGCGCGCCGCCACCTTACAGCAGAGGTCATCGGCCACTTACC CGGGGTCCTCTTCCAGC	1148
Db	128083	AGGGGCGCGCCGCCACCTTACAGCAGAGGTCATCGGCCACTTACC CGGGGTCCTCTTCCAGC	1280244
OY	1149	ACACGACAGCAGTGGGGCGCCCTCTCTCTGAGGGAGACCGGGCTCCACACACACACACAC	1208
Db	128023	ACACGACAGCAGTGGGGCGCCCTCTCTCTCTGAGGGAGACCGGGCTCCACACACACACACAC	1279644
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Db	127963	TGCGCGCCCTTAGAGAGCGCAGCCATCTGGAGACAAGAGAAAGATTAACAGAAAGACACC	1279044
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Db	127903	CTCTCTTAGAGGTCCCAAGGGGGGGCGGGCTGGGGGCTGCTAGGTGAAAAGGACAG	127851

Db	947	GCACCCACCATCTTCGCTGTTCAGACGGGGAGAGAGACCCCCACCTTACCAAGGGCCCCCTTCAC	1006
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Db	1007	CTCTCAGCTTCGGAGACCCCGAGCAGCAGCTGGAAGTGAACCGGGAGTTCGGTGCAGGCACC	1066
QY	970	CCCAAGACGAAACCATCTTCGACAGTGAACCTGATGGATAGTCCAGGCTGGGGCCCCCTG	1029
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QY	1030	CCCCCCAGCAGTAACTTCGGGCTATCAGCGCCACAGTGTCTAGGGCAGCGGGGGCCGATGGA	1089
Db	1127	CCCCCCAGCAGTAACTTCGGGCTATCAGCGCCACAGTGTCTAGGGCAGCGGGGGCCGATGGA	1186
QY	1090	GGGGCCGCGCCGCCACCTTACAGCAGGAGTATCGGCCACTACCCGGGGTCTCTTCCAGCA	1149
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QY	1150	CCAGCAGACGAGTGGGGCGCCCTCTCTTCTGTAAGGGGACCGCGTCCACACACACAT	1209
Db	1247	CCAGCAGACGAGTGGGGCGCCCTCTCTTCTGTAAGGGGACCGCGTCCACACACACAT	1306
QY	1210	CGCGCCCTTAGAGAGCCGACGCTATCTGGAGGAAAGAAAGATTAACAGAAAGACACC	1269
Db	1307	CGCGCCCTTAGAGAGCCGACGCTATCTGGAGGAAAGAAAGATTAACAGAAAGACACC	1366
QY	1270	TCTTAGGGTCCCAAGGGG 1289	
Db	1367	TCTTAGGGTCCCAAGGGG 1386	

RESULT 9			
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LOCUS		1583 bp	DNA
DEFINITION	Sequence 32 from Patent WO0242776.	linear	PAT 13-FEB-2003
ACCESSION	AX593655		
VERSION	AX593655.1	GI:28375034	
KEYWORDS			
SOURCE	Homo sapiens (human)		

ORGANISM	REFERENCE
Homo sapiens	1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
Sun, Y., Recipon, H., Chen, S. Y., and Liu, C.	
Compositions and methods relating to prostate specific genes and proteins	
Patent: WO 0242776-A 32 30-MAY-2002;	

FEATURES	Location/Qualifiers
source	1..1583

BASE COUNT	361 a	469 c	457 g	296 t
ORIGIN				

Query Match	42.4%	Score 560	DB 6	Length 1583
Best Local Similarity	100.0%	Prid. No. 1.1e-277		
Matches 560	Conservative 0	Mismatches 0	Indels 0	Gaps 0

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Db 827 GCCGAGGCTACGCCCCCGCCTCGGCCACAGGACGGCTTGGCGTGGCCGCGCCCTTCGCCCA 886

790 GCGGAGCGCTTCCACCGCTTCCAGCCCACTATCCGTAAGCTGAGCAGAGATCGACCT 849

Db 887 GCGGACGCGTTCACCGCTTCAGCCCACTATCGTACTGACAGCAGAGATCGACT 946

850 GCCACCCACCATCTTCGCTGCAGACGGGGAGGACCCCCACCCCTTACACAGGGCCCCCTGGAC 909

RESULT 10	
HSJ1059L7/c	
LOCUS	HSJ1059L7 150224 bp DNA linear PRI 24-FEB-2001
DEFINITION	Human DNA sequence from clone Rp5-1059L7 on chromosome 20q13.2-13.3 Contains the 5' end of the TMEPAI (PMEPAI) gene encoding an androgen induced 1b transmembrane protein, ESTs, STSS, GSSS and two Cpg islands, complete sequence.
ACCESSION	A1121913
VERSION	A1121913.4 GI:7161781
KEYWORDS	HNG; CpG island; PMEPAI; TMEPAI; transmembrane protein.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 150224) Skuce,C.
AUTHORS	Direct Submission
TITLE	Submitted (23-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
JOURNAL	C810 ISA, UK. E-mail enquiries: humquerry@sanger.ac.uk
COMMENT	requests: clonerequests@sanger.ac.uk On Mar 6, 2000 this sequence version replaced gi:7007305.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em1, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/genp/chr10>
This sequence is the entire insert of clone RP5-1059L7. The true left end of clone RP11-402F1 is at 106677 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP5-1059L7 is from the library RPc1-5 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pCYPAC2.

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Location/Qualifiers

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QY      1005 ATAGTCCAGAGCTGGCGGCCCCCTGCCCCAGCAGTAACTCGGCATCAGCGCAGT 1064
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Db      407  GCTACGCGCAGCGCGCGCGCGCATGAGAGGCGCGCGCCACCTTACAGCAGATCAGGCC 348
QY      1125 ACTACCGGCGGCTCTCTTCAGACACAGCAGAGCAGTGGGCGCGCTCTCTCTGAGG 1184
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1185 GG 1186
287 GG 286

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DEFINITION Sequence 107 from Patent WO955858.
ACCESSION AX011709
VERSION  AX011709.1 GI:9998233
KEYWORDS
SOURCE  Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
          Pliarsky,C.
TITLE    Human nucleic acid sequences obtained from pancreas tumor tissue
JOURNAL  Patent: WO 955858-A 107 04-NOV-1999;
          SCHMITT ARMINT (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
          BERND (DE); ROSENTHAL ANDRE (DE); METZEN GENES FUER GENOMFORSCHUN
          (DE); PLIARSKY CHRISTIAN (DE)
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Matches 321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      426  TCACGTGCTGCTGACCACTATCAAGCTGTCTCAGAGGTCCTTCATCAGCCGCGCACACC 485
QY      645  AGGGGGGAGAGAGAAGATGCTCTGCTCAGAGAGATGCTGTGGCCCTCGGAGAGCA 704
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Db      546  CAGTGTCAAGCAAGCATCCAGAGCCGAGCTTACGCGCCGCTCGGCGCCACGAGAC 605
QY      765  GCTTGGCGCTGCGCGCTTGTGCGCAGCGGAGAGCGCTTCCACCGCTTCCACCGCACTATC 824
Db      606  GCTTGGCGCTGCGCGCTTGTGCGCAGCGGAGAGCGCTTCCACCGCTTCCACCGCACTATC 665
QY      825  CGTACTGACGACGAGATGACCTGCAACCAATCTGCTGACGAGGGAGAGAGC 884

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Db      666  CGTACTGACGACGAGATGACCTGCGCCGACCATCTGCTGTCCAGAGGGAGAGAC 725
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RESULT 14
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DEFINITION Sequence 495 from Patent WO0151670.
ACCESSION AX199565
VERSION  AX199565.1 GI:15389996
KEYWORDS
SOURCE  Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Shinkets,R.A. and Leach,M.D.
TITLE    Nucleic acids containing single nucleotide polymorphisms and
          methods of use thereof
JOURNAL  Patent: WO 0151670-A 495 19-JUL-2001;
          Curagen Corporation (US)
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ORIGIN

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Db      1    CACGTCCTTCATCAGCCGCGCAGCAGCGGCGGAGAGAGAGATGCC 51

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RESULT 15
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DEFINITION Mus musculus Nedd4 WW domain-binding protein 4 mRNA, partial cds.
ACCESSION AF220208
VERSION  AF220208.1 GI:12004973
KEYWORDS
SOURCE  Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
          1 (bases 1 to 651)
          Jolliffe,C.N., Harvey,K.F., Haines,B.P., Parasivam,G. and Kumar,S.
          Identification of multiple proteins expressed in murine embryos as
          binding partners for the WW domains of the ubiquitin-protein ligase
          Nedd4
          Biochem. J. 351 Pt 3, 557-565 (2000)
JOURNAL  MEDLINE 20498735
PUBMED  11042109
REFERENCE 2 (bases 1 to 651)
AUTHORS Jolliffe,C.N. and Kumar,S.
TITLE    Direct Submission
JOURNAL  Submitted (30-DEC-1999) Division of Haematology, Hanson Centre for
          Cancer Research, IMVS, Frome Rd, Adelaide, SA 5000, Australia
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2003, 20:09:06 ; Search time 416 Seconds
(without alignments)
8572.014 Million cell updates/sec

Title: US-09-934-249-1

Perfect score: 1321
Sequence: 1 cgaccgcgcttcgagcga.....ctgcgtagtgtaaaagcag 1321

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Database size: 8

Total number of hits satisfying chosen parameters: 2877269

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1321	100.0	1321	24	ABK12137 Human cDNA encodin
2	800	60.6	1140	24	ABK92120 Prostate cancer as
3	788	59.7	1066	22	AA157868 Human polynucleoti
4	749	56.7	969	21	AAA75151 cDNA encoding a hu
5	749	56.7	1061	21	AAAA47429 Sequence encoding
6	744	56.7	1334	25	AB236103 Human secretory po
7	744	56.3	969	21	AAA75153 cDNA clone encodin
8	698	52.8	969	21	AAA75164 cDNA clone encodin

9	698	52.8	969	21	AAA75165	cDNA clone encodin
10	560	42.4	1583	24	ABK51424	Prostate specific
11	401	30.4	408	22	AA65983	Novel human polynu
12	394	29.8	1069	22	AA159654	Human polynucleoti
13	364	27.6	474	25	AB284732	Toxicologically re
14	302	22.9	693	24	ABK12143	Human MIVR-1 homol
15	271	20.5	812	20	AA252964	Human prostate tum
16	229	17.3	254	21	AAA41265	Human secreted exp
17	106	8.0	1879	23	AA584503	DNA encoding novel
18	63	4.8	426	23	AA584502	DNA encoding novel
19	60	4.5	60	24	ABN40872	Human spliced tran
20	56	4.2	522	24	ABT10027	Human breast cance
21	51	3.9	51	22	AAH89714	Human coding sequ
22	45	3.4	837	24	ABQ43500	Oligonucleotide fo
23	45	3.4	837	24	ABQ43501	Oligonucleotide fo
24	44	3.3	878	24	ABK12142	Mouse cDNA encodin
25	44	3.3	1713	21	AAA75152	cDNA encoding a mu
26	44	3.3	1713	21	AAA75166	cDNA clone encodin
27	44	3.3	1713	21	AAA75167	cDNA clone encodin
28	44	3.3	1713	21	AAA75168	cDNA clone encodin
29	42	3.2	673	24	ABT09178	Phase-1 Rat CT gen
30	41	3.1	475	24	ABK12144	Human MIVR-1 homol
31	37	2.8	837	24	ABQ43498	Oligonucleotide fo
32	37	2.8	837	24	ABQ43499	Oligonucleotide fo
33	34	2.6	640	21	AA656015	Human breast cell
34	32	2.4	577	22	ABA50270	Human foetal liver
35	32	2.4	577	22	ABA68210	Human brain expres
36	32	2.4	577	22	ABA35222	Human bone marrow
37	32	2.4	577	22	AAK16592	Probe #13051 for g
38	32	2.4	577	22	AAK42346	Probe #17111 used t
39	32	2.4	577	22	AAI23118	Human liver single
40	32	2.4	577	22	AAI48425	Human genome-deriv
41	32	2.4	577	23	AAI08772	Human breast cell
42	32	2.4	577	23	AB541955	Human foetal liver
43	32	2.4	577	24	AB516402	Human breast cell
44	32	2.4	1964	22	ABA45134	Human
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ALIGNMENTS

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AC	05-JUN-2002	(first entry)
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XX		
KW	Human; ss; gene; MIVR-1; Mechanically Induced Vascular Receptor 1;	
KW	cytostatic; cardiant; cerebroprotective; antiarteriosclerotic;	
KW	cardiac cell; anti-apoptotic; vascular endothelial cell;	
KW	cardiac hypertrophy; myocardial infarction; stroke; arteriosclerosis;	
KW	heart failure.	
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OS	Homo sapiens.	
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PN		
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PD	28-FEB-2002.	
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PF	21-AUG-2001; 2001WO-US26089.	
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PR	22-AUG-2000; 2000US-227159P.	

XX	(BCHM) BRIGHAM & WOMENS HOSPITAL INC.
PA	(PRIZ) PEIZER INC.
PI	
PI	Lee RT, Landschultz KT, Kennedy SP, Thompson JF, Turi TG;
XX	
DR	WPI; 2002-280912/32.
DR	P-PSDB; AAU78231.
XX	
PT	Novel nucleic acid molecule encoding Mechanically Induced Vascular
PT	Receptor-1 polypeptide, useful for treating cardiovascular diseases
XX	
PS	Claim 2; Page 87-88; 105pp; English.
XX	
CC	The invention relates to an isolated nucleic acid molecule encoding a
CC	Mechanically Induced Vascular Receptor (MYR)-1 polypeptide having
CC	cardiac cell anti-apoptotic activity and fragments of it provided
CC	they are not identical to Genbank sequences AT76141.1, A1594390,
CC	NM_004338 and A0177461. Also included are expression vectors, host
CC	cells, the MYR-1 polypeptide, MYR-1 binding peptides, modulators of
CC	MYR-1, contacting a molecule having cardiac cell anti-apoptotic activity
CC	with a candidate agent, where the molecule is a nucleic acid molecule
CC	comprising MYR-1, IEX-1, VDUP-1, Brg-2 and Trs-1ld or its
CC	expression product, determining if the anti-apoptotic activity is
CC	modulated and thereby identifying a modulator. The cardiac cell anti-
CC	apoptotic molecules and nucleic acids of the invention are useful for
CC	treating, diagnosing and monitoring progression of such diseases and
CC	disorders as characterised by increased apoptotic cell-death of vascular
CC	endothelial cells e.g. cardiac hypertrophy, myocardial infarction,
CC	stroke, arteriosclerosis and heart failure. The present sequence
CC	encodes human MYR-1.
CC	
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DB	121 GCGGCGAAGCGGCGCGCGCGGTGTCAGAGCCATTTTCCGAGAGCGCACCGCGGGCATGCGG 180
OY	181 AGCGCGCGGGGGGCTCGAGAGGAGAGCGGGGGGCGAGAGCGAGCGGTCGCCGCAGC 240
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DB	241 TGAGCGCGCGCGCGCGCGGGAATTGGCGGCGAGCCGAGCGCGCGAGCGGGGCGGC 300
OY	301 CTCCCCTCCGCGCGCGCTCTGTCAGATGCGGGGCGCCAGTCTCGGGGCGCGCGAGCCCC 360
DB	301 CTCCCCTCCGCGCGCGCTCTGTCAGATGCGGGGCGCCAGTCTCGGGGCGCGCGAGCCCC 360
OY	361 CCCCGCGCGCGCGCGAGCG 420
DB	361 CCCCGCGCGCGCGCGAGCG 420
OY	421 CTGTATGGGGGTCAAACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
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PN W0200230268-A2.
 XX 18-APR-2002.
 XX 12-OCT-2001; 2001WO-US32045.
 XX 13-OCT-2000; 2000US-0687576.
 PR 08-DEC-2000; 2000US-0733288.
 PR 08-DEC-2000; 2000US-0733742.
 PR 24-JAN-2001; 2001US-263957P.
 PR 16-MAR-2001; 2001US-276791P.
 PR 16-MAR-2001; 2001US-276888P.
 PR 06-APR-2001; 2001US-281922P.
 PR 24-APR-2001; 2001US-286214P.
 PR 30-APR-2001; 2001US-0847046.
 PR 04-MAY-2001; 2001US-288589P.
 XX
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 XX Gish RC, Mack DH, Wilson KE, Afar D, Hevezl P;
 DR MPI: 2002-471335/50.
 P-PSDB: ABG61805.

PT Detecting a prostate cancer-associated transcript in a cell in a
 PT patient, useful for diagnosing prostate cancer (PC) or screening
 PT modulators of PC, by determining if prostate cancer-associated genes
 PT are expressed in a prostate tissue
 PS
 PS Claim 22; Page 305; 436pp; English.

CC The present invention relates to methods of detecting a prostate
 CC cancer-associated transcript in a cell from a patient. The method
 CC comprises contacting a biological sample from the patient with
 CC prostate cancer-associated polynucleotides (designated PC genes) that
 CC selectively hybridize to a sequence that is at least 80% identical
 CC to them. The prostate cancer-associated polynucleotide sequences
 CC are differentially expressed in prostate tumour tissue or in
 CC prostate cancer and are derived from the tissues of various
 CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
 CC The methods of the invention are useful for diagnosing and treating
 CC prostate cancer in mammals. The prostate cancer-associated genes are
 CC useful for diagnosing or treating prostate cancer, as well as for
 CC identifying modulators of prostate cancer or agents that inhibit
 CC prostate cancer. The nucleic acid sequences are particularly useful
 CC in gene therapy, as a vaccine or in antisense applications.
 CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
 CC sequences.

Sequence 1140 BP; 270 A; 350 C; 336 G; 184 T; 0 other;

Query Match 60.6%; Score 800; DB 24; Length 1140;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 522 CGAGAGCTGGAGTTGTCAGATCATCATCTGCTGCTGATGATGATGATGATG 581
 DB 100 CGAGAGCTGGAGTTGTCAGATCATCATCTGCTGCTGATGATGATGATGATG 159
 DB 160 TGATCAGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATG 219
 QY 582 TGATCAGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATG 641
 DB 642 GCGAGGGGCGAGAGAGATGATGATGATGATGATGATGATGATGATGATG 701
 DB 220 GCGAGGGGCGAGAGAGATGATGATGATGATGATGATGATGATGATGATG 279
 QY 702 GCACAGTGTACAGCAAGCAATCCAGAGCGCAGGTCTAGCCCGCTCGGCCACG 761
 DB 280 GCACAGTGTACAGCAAGCAATCCAGAGCGCAGGTCTAGCCCGCTCGGCCACG 339
 QY 762 ACCGCTGCGCTGCGCTTCCGCGAGCGGAGCGCTTCCAGCGCTTCCAGCGC 821

DB 340 ACCGCTGCGCTGCGCTTCCGCGAGCGGAGCGCTTCCAGCGCTTCCAGCGC 399
 QY 822 ATCCGCTACCTGACAGAGATGATGATGATGATGATGATGATGATGATGATG 881
 DB 400 ATCCGCTACCTGACAGAGATGATGATGATGATGATGATGATGATGATGATG 459
 QY 882 AGCCCGCACCTTACAGAGGCGCTGACACCTTCCAGCTTCCAGCTTCCAGCTT 941
 DB 460 AGCCCGCACCTTACAGAGGCGCTGACACCTTCCAGCTTCCAGCTTCCAGCTT 519
 QY 942 AACTGAAACCGGAGTGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1001
 DB 520 AACTGAAACCGGAGTGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 579
 QY 1002 TGGATAGTGGAGGCTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1061
 DB 580 TGGATAGTGGAGGCTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 639
 QY 1062 CGTGTACGAGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1121
 DB 640 CGTGTACGAGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 699
 QY 1122 GCCACTACCGCGGCTCTCTTCCAGCACACAGAGAGAGAGAGAGAGAGAG 1181
 DB 700 GCCACTACCGCGGCTCTCTTCCAGCACACAGAGAGAGAGAGAGAGAGAG 759
 QY 1182 AGGGAGCGCGCTCCACACACACACACACACACACACACACACACACACAC 1241
 DB 760 AGGGAGCGCGCTCCACACACACACACACACACACACACACACACACACAC 819
 QY 1242 AAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1301
 DB 820 AAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 879
 QY 1302 CTGCTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1321
 DB 880 CTGCTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 899

RESULT 3
 ID AA157868 standard; cDNA; 1066 BP.
 XX AA157868;
 AC 22-OCT-2001 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 71.
 XX
 KW Human; noctropic; immunosuppressant; cytoskeletal; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia; ss.
 XX
 OS Homo sapiens.
 PN W0200153312-A1.
 XX 26-JUL-2001.
 PF 26-DEC-2000; 2000WO-US34263.
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX

XX	(HYSE-) HYSEQ INC.
XX	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI	Meng J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI	Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX	WPI: 2001-442253/47.
DR	P-PsDB; AAM38712.
XX	
PT	Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
PS	Claim 1; SEQ ID NO 71; 10078pp; English.
XX	
CC	The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukemias and C.N.S. disorders.
CC	Note: The sequence data for this patent did not form part of the printed specification.
CC	
XX	
SQ	Sequence 1066 BP; 225 A; 348 C; 325 G; 168 T; 0 other:
	Query Match 59.7%; Score 788; DB 22; Length 1066; Best Local Similarity 100.0%; Pred. No. 0; Matches 788; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	534 TTGTCACATCATCATCGTGTGGTGAGTAGTAGTGATGTGTGTATCACTGCC 593
DB	125 TTGTCACATCATCATCGTGTGGTGAGTAGTAGTGATGTGTGTATCACTGCC 184
OY	594 TGCTAGGCACATCAACAAGCTGTGTGAGCGGTCTTCATCAGCGCCAGCAGGAGGCGGA 653
DB	185 TGCTAGGCACATCAACAAGCTGTGTGAGCGGTCTTCATCAGCGCCAGCAGGAGGCGGA 244
OY	654 GGAGAAGAGATGCCCTGTCTCAGAAGATGCTGTGGCCCTCGAGAGCAACTGTGTAC 713
DB	245 GGAGAAGAGATGCCCTGTCTCAGAAGATGCTGTGGCCCTCGAGAGCAACTGTGTAC 304
OY	714 GCACAGGAATCCCAAGGCGGAGCTPACGGCCCGCTCGGCGCCACGACGCGTGGCGG 773
DB	305 GCACAGGAATCCCAAGGCGGAGCTPACGGCCCGCTCGGCGCCACGACGCGTGGCGG 364
OY	774 TGCGCCCTTTCCGCCAGCGGGAGCGCTTCACCGCTTCAGGCCACATCCGTACGTGC 833
DB	365 TGCGCCCTTTCCGCCAGCGGGAGCGCTTCACCGCTTCAGGCCACATCCGTACGTGC 424
OY	834 ACACAGAGATTCACCTGCGCACACCACACATCTGCTGTCAAGAGGGAGAGGCCGCCACCT 893
DB	425 ACACAGAGATTCACCTGCGCACACCACACATCTGCTGTCAAGAGGGAGAGGCCGCCACCT 484
OY	894 ACCAGAGGCCCTCGCAACCTCTCAGCTTCGGGACCCCGAGAGAGCAGCTGGAATGAACGAGG 953
DB	485 ACCAGAGGCCCTCGCAACCTCTCAGCTTCGGGACCCCGAGAGAGCAGCTGGAATGAACGAGG 544
OY	954 AGTCGGTGGCGGACCCCCAAAACAGAACCATCTTGACAGTAACCTGATGATGATGATGCA 1011
DB	545 AGTCGGTGGCGGACCCCCAAAACAGAACCATCTTGACAGTAACCTGATGATGATGATGCA 604
OY	1014 GGCTGGGCGGCCCTGCCCGCAGAGTAAGTCCGGGCTACAGCGCACGTCTACAGGCA 1072
DB	605 GGCTGGGCGGCCCTGCCCGCAGAGTAAGTCCGGGCTACAGCGCACGTCTACAGGCA 664

QY	1074	CGCGCGGGCGCGATGGAGGGGGCGCGCGCCAGCCTTACAGAGATCATGCGCCACTATCCGG	1133
Db	665	GGCGCGGGCGCGATGGAGGGGGCGCGCGCCAGCCTTACAGAGATCATGCGCCACTATCCGG	724
OY	1134	GGTCTCTCTCTCCACACACAGCAGAGCAGTGGGGCGCCCTCTCTCTCTGGAGGGAGCCGGC	1193
Db	725	GGTCTCTCTCTCCACACACAGCAGAGCAGTGGGGCGCCCTCTCTCTGGAGGGAGCCGGC	784
OY	1194	TTCCACACACACACATGCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCAGAAAGAGAAGATA	1253
Db	785	TTCCACACACACACATGCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCAGAAAGAGAAGATA	844
OY	1254	AACAGAAAGAGACACCTCTCTTCTAGGGGTCCCGCAGGGGGCGCGGCTGTGGGCTGTA	1313
Db	845	AACAGAAAGAGACACCTCTCTTAGGGGTCCCGCAGGGGGCGCGGCTGTGGGCTGTA	904
OY	1314	AAAGGCAG 1321	
Db	905	AAAGGCAG 912	
RESULT 4			
AAAT5151	ID	AAAT5151 standard; cDNA, 969 BP.	
AAAT5151;	AC		
15-JAN-2001	DT	(first entry)	
CDNA	DE	encoding a human TANGO 261 polypeptide.	
TANGO 266;	XX	TANGO 216;; TANGO 261; TANGO 262; TANGO 267;	
cellular proliferation;	KW	cellular differentiation; cellular adhesion;	
von Willebrand factor-associated disorder;	KW	cell trafficking; cancer;	
hematopoietic associated disease; atelectasis;	KW	pulmonary congestion;	
oedema; emphysema; chronic bronchitis;	KW	bronchial asthma; bronchiectasis;	
intestinal disorder; spleen associated disease;	KW	renal disorder;	
cardiovascular disorder; ischemic heart disease;	KW	hydrocephalus;	
brain herniation; tatarogenic disease; inflammation;	KW	meningitis;	
Alzheimer's Disease; cerebral toxoplasmosis;	KW	Parkinson's disease;	
multiple sclerosis; hydrocephalus; encephalitis;	KW	hepatic disorder; ss.	
Homo sapiens.	OS		
key	PH	location/Qualifiers	
CDS	FT	6..764	
FT	FT	/tag= a	
FT	FT	/product= "TANGO 261"	
FT	FT	6..89	
FT	FT	/tag= b	
FT	FT	90..764	
FT	FT	/tag= c	
WO200052022-A1.	XX		
08-SEP-2000.	XX		
01-MAR-2000; 2000MO-US05226.	XX		
01-MAR-1999; 99US-0122458.	XX		
(MILL-) MILLENNIUM PHARM INC.	XX		
Barnes TM, Holtzman DA, Sharp JD, Fraser CC;	XX		
WPI; 2000-579269/54.	XX		
P-PSDB; AAB18449.	XX		
Novel human and murine secreted proteins designated TANGO 216, 261,	XX		
262, 266 and 267 useful as modulating agents of cellular processes,	XX		
e.g. for treating cancer -	XX		
Claim 2; Fig 5; 175pp; English.	XX		

XX The present sequence encodes a human TANGO 261 polypeptide. The
 CC specification also describes TANGO 266, TANGO 216, TANGO 262, and
 CC TANGO 267. The TANGO polypeptides can be used to modulate cellular
 CC proliferation, modulate cellular differentiation and/or modulate
 CC cellular adhesion. The proteins can be used to treat any von Willebrand
 CC factor-associated disorder, regulate extracellular matrix structuring,
 CC cellular adhesion, and cell trafficking and/or migration, modulate
 CC cellular interactions, modulate cell adhesion in proliferative
 CC disorders, such as cancer, modulate the proliferation, differentiation,
 CC and/or function of cells that appear in the bone marrow, and leukocytes,
 CC treat bone marrow, blood and hematopoietic associated diseases and
 CC disorders, atelectasis, pulmonary congestion or edema, emphysema,
 CC chronic bronchitis, bronchial asthma and bronchiectasis, intestinal
 CC disorders, spleen associated diseases, modulate renal disorders, treat
 CC cardiovascular disorders such as ischemic heart disease, modulate the
 CC proliferation, differentiation, and/or function of bone and cartilage
 CC cells and to treat bone and/or cartilage associated diseases or
 CC disorder. They may also be used to treat disorders associated with the
 CC ovaries, cerebral edema, hydrocephalus, brain herniations, iatrogenic
 CC disease, inflammation, bacterial and viral meningitis, Alzheimer's
 CC disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis,
 CC brain cancers, hydrocephalus and encephalitis, and treat hepatic
 CC disorders.

50 Sequence 969 BP; 211 A; 316 C; 294 G; 148 T; 0 other;

Query Match 56.7%; Score 749; DB 21; Length 969;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 799; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 522 CGAGCTGAGATGTTGTCAGATCATCATCTGCTGCTGATGATGCTGATGCTGCTG 581
 DB 10 CGGAGCTGAGATGTTGTCAGATCATCATCTGCTGCTGATGATGATGATGCTGCTG 69
 QY 582 TGATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 641
 DB 70 TGATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 129
 QY 642 GCCAGGGGCGAGAGAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 701
 DB 130 GCCAGGGGCGAGAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 189
 QY 702 GCACAGTGTACAGCAAGCAATCCACAGCCGAGCTGTACGCCCGCTGCGCCACCG 761
 DB 190 GCACAGTGTACAGCAAGCAATCCACAGCCGAGCTGTACGCCCGCTGCGCCACCG 249
 QY 762 ACCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 821
 DB 250 ACCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 309
 QY 822 ATCCGTAATCTGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 881
 DB 310 ATCCGTAATCTGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 369
 QY 882 AGCCGCCACCTTACAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 941
 DB 370 AGCCGCCACCTTACAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 429
 QY 942 AACGTAACCGGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1001
 DB 430 AACGTAACCGGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 489
 QY 1002 TGATATAGTGTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1061
 DB 490 TGATATAGTGTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 549
 QY 1062 CGTGTCTAGCGAGCGGCGGCGCATGAGAGGCGCGCGCCACCTTACAGAGGCTGCTG 1121
 DB 550 CGTGTCTAGCGAGCGGCGGCGCATGAGAGGCGCGCGCCACCTTACAGAGGCTGCTG 609
 QY 1122 GCCACTACCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1181

DB 610 GCCACTACCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 669
 QY 1182 AGGGAGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1241
 DB 670 AGGGAGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 729
 QY 1242 AAGGAAGGATTAACAGAAAGAGACCCCTGCTGAGGTGCCAGGGGGCGGCTGAGG 1301
 DB 730 AAGGAAGGATTAACAGAAAGAGACCCCTGCTGAGGTGCCAGGGGGCGGCTGAGG 789
 QY 1302 CTGCTGAGGTGTAAGAGCAG 1321
 DB 790 CTGCTGAGGTGTAAGAGCAG 809

RESULT 5

AAAA7429

AAAA7429 standard; DNA; 1061 BP.

AAAA7429; 20-OCT-2000 (first entry)

Sequence encoding human neuron-associated protein.

XX Neuron associated protein; NEUP; neurological disorder; epilepsy;
 KW ischemic cerebrovascular disease; stroke; cerebral neoplasm;
 KW Alzheimer's disease; Pick's disease; Huntington's disease;
 KW dementia; Parkinson's disease; demyelinating disease; meningitis;
 KW prion disease; Kuru; Creutzfeldt-Jakob disease; neurofibromatosis;
 KW cerebral palsy; muscular dystrophy; central nervous system;
 KW acinic keratosis; arteriosclerosis; atherosclerosis; bursitis;
 KW cirrhosis; hepatitis; mixed connective tissue disease; MCTD;
 KW myelofibrosis; paroxysmal nocturnal haemoglobinuria; cancer;
 KW autoimmune disease; inflammation; acquired immunodeficiency syndrome;
 KW AIDS; Addison's disease; adult respiratory distress syndrome;
 KW allergy; ankylosing spondylitis; amyloidosis; anaemia; asthma;
 KW Werner syndrome; trauma; human; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH 101..859
 FT /*tag= a
 FT /product= Neuron associated protein

XX WO200034477-A2.

XX 15-JUN-2000.

XX 10-DEC-1999; 99WO-US30408.

XX 11-DEC-1998; 98US-0210083.

XX 11-DEC-1998; 98US-9123456.

XX 09-FEB-1999; 99US-0119365.

XX 16-MAR-1999; 99US-0124687.

XX (INCYT) INCYTE PHARM INC.

XX Tang YF, Yue H, Baughn MR, Hillman JL, Lai P, Au-young J, Yang J;

XX Lu DAW, Azimzal Y;

XX WPI; 2000-423423/36.

XX P-PSDB; AAB01388.

XX New human neuron-associated proteins and polynucleotides encoding them,
 XX useful for diagnosis, treatment and prevention of cell proliferative
 XX disorders including cancer, neuronal and neurological disorders
 XX Claim 9; Page 136; 145pp; English.
 XX Human neuron-associated proteins (NEUP) can be used for for

treating or preventing a disorder associated with decreased expression or activity of NEUP. Antagonists of NEUP are useful for treating or preventing disorder associated with increased expression or activity of NEUP. NEUP or their fragments or derivatives are useful for treating neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia and Parkinson's disease. NEUPs are also useful for treating other demyelinating diseases, bacterial and viral meningitis, prion diseases including kuru, Creutzfeldt-Jakob disease, nutritional and metabolic diseases of the nervous system, neurofibromatosis, other developmental disorders of the central nervous system, cerebral palsy, neuromuscular disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, inherited, metabolic, endocrine, and toxic myopathies, mental disorders including mood, anxiety and schizophrenic disorders, a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, and an autoimmune/inflammatory disorder such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal parasitic, protozoal, and helminthic infections, and trauma. This sequence was given the Incyte ID no. 1871286CBL.

Sequence 1061 BP: 225 A; 342 C; 326 G; 168 T; 0 other;

Query Match	Similarity	Score	749;	DB	21;	Length	1061;
Best Local	99.98;	Pred.	0;				
Matches	799;	Conservative	0;	Mismatches	1;	Indels	0;
						Gaps	0;
QY	522	CGGAGCTGGAGTTTGTTCAGATCATCATCGTGTGTGTGATGATGATGATGATG	581				
DB	105	CGGAGCTGGAGTTTGTTCAGATCATCATCGTGTGTGTGATGATGATGATGATG	164				
QY	582	TGATTCAGTGGCTGCTGAGCCACATCAAGCTGTGTGACGGTCCCTTATCGAGCGGACA	641				
DB	165	TGATTCAGTGGCTGCTGAGCCACATCAAGCTGTGTGACGGTCCCTTATCGAGCGGACA	224				
QY	642	GCCAGGGGCGGAGAGAGAAATACCCCTGTCTTACAGAAAGATGTGCTGTGAGGAG	701				
DB	225	GCCAGGGGCGGAGAGAGAAATACCCCTGTCTTACAGAAAGATGTGCTGTGAGGAG	284				
DB	702	GCACAGTGTGAGGACAGGAATCCACAGCCGACAGTGTACGCCCGCTGTGCGCCACCG	761				
DB	285	GCACAGTGTGAGGACAGGAATCCACAGCCGACAGTGTACGCCCGCTGTGCGCCACCG	344				
QY	762	ACCGCTGTGGCGCTGGCGCCCTTCCGCCAGGGGAGCGCTTCCAGCGTCCAGGCCACCT	821				
DB	345	ACCGCTGTGGCGCTGGCGCCCTTCCGCCAGGGGAGCGCTTCCAGCGTCCAGGCCACCT	404				
QY	822	ATCCGTACCTGCAGCAGCAGATTCGACCTGCACACCACCATCTCGCTGTACAGCGGGAGG	881				
DB	405	ATCCGTACCTGCAGCAGCAGATTCGACCTGCACACCACCATCTCGCTGTACAGCGGGAGG	464				
QY	882	AGCCCCACACCTACCGAGGCGCCCTGCACCTTCACGCTTGGGAGCCCGAGCAGCAGCTGG	941				
DB	465	AGCCCCACACCTACCGAGGCGCCCTGCACCTTCACGCTTGGGAGCCCGAGCAGCAGCTGG	524				
QY	942	AACGTAAACCGGAGAGTCGTGGCGGACGCCCAAGAAAGCAATCTTGACAGTGCACCTGA	1001				
DB	525	AACGTAAACCGGAGAGTCGTGGCGGACGCCCAAGAAAGCAATCTTGACAGTGCACCTGA	584				
QY	1002	TGGATAGTGCAGGCTGGGCGGCGCCCTCCGCCAGCAGTAACTCGGCGATCAGCGCCA	1061				
DB	585	TGGATAGTGCAGGCTGGGCGGCGCCCTCCGCCAGCAGTAACTCGGCGATCAGCGCCA	644				
QY	1062	CGGTGTACGGCAGCGCGGGCGCATGAGAGGGCGCGGCCCATCTACACGAGGTATCG	1121				

Accession	Sequence	Position
D8	CGTGGTACGGCAGCGCGGGCGCATGGAGGGGCCGCCACCTCAACAGAGTATCG	704
QY	1122 GGCACATACCCGGGGTCTCTCTTCAGACACAGCAGACAGTGGGCGCCCTCTCTGTGG	1181
D8	705 GGCACATACCCGGGGTCTCTCTTCAGACACAGCAGACAGTGGGCGCCCTCTCTGTGG	764
QY	1182 AGGGGACCCGGCTCCACACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCA	1244
D8	765 AGGGGACCCGGCTCCACACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCA	824
QY	1242 AAGAGAAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCTCCCAAGGGGGCGGGCTGGGG	1301
D8	825 AAGAGAAAGGATAAACAGAAAGGACACCCTCTCTAGGGTCTCCCAAGGGGGCGGGCTGGGG	884
QY	1302 CTGCGTAGGTGAAAAGGCGAG 1321	
D8	885 CTGCGTAGGTGAAAAGGCGAG 904	

Accession	Gene	Species	Source	Accession	Gene	Species	Source
AB236103	AB236103	standard	CDNA	1334	BP		
AB236103	AB236103						
10-FEB-2003	(first entry)						
Human secretory polynucleotide	SPM	SEQ ID NO 267					
Human: SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia							
asthma; Crohn's disease; neurological disorder; epilepsy; cancer							
Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;							
multiple sclerosis; Parkinson's disease; cell proliferative disorder;							
anti-inflammatory; immunosuppressive; neuroprotective; neotropic;							
neurologic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic;							
antiproliferative; antianemic; anti-HIV; human immunodeficiency virus;							
secretory polynucleotide; secretory protein; gene; ss							
Homo sapiens							
MO200283876-A2							
24-OCT-2002							
27-MAR-2002; 2002MO-0509921							
29-MAR-2001; 2001US-280667P							
29-MAR-2001; 2001US-280668P							
16-MAY-2001; 2001US-281280P							
17-MAY-2001; 2001US-281829P							
17-MAY-2001; 2001US-291849P							
19-JUN-2001; 2001US-299428P							
20-JUN-2001; 2001US-299776P							
20-JUN-2001; 2001US-300001P							
(INCYTE) INCYTE GENOMICS INC							
Duffo A, Jones AL, Tran AB, Dahl CR, Gletzen D, Chinn J,							
Dufour GE, Hillman JL, Yu JY, Tzason O, Yap PE, Amhey SR,							
Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;							
Perilla CH, David MH, Lewis SA, Panzer AJ, Panzer SR, Harris B,							
Flores V, Marwaha R, Lo A, Ian RY, Urashka ME;							
WPI; 2003-075543/07							
P-PSDB; ABP75660							
New human secretory proteins and polynucleotides, useful for							
diagnosing, treating or preventing autoimmune/inflammatory disorders							
(e.g. AIDS), neurological disorders (e.g. Alzheimer's), or cell							
proliferations or cancers							
Claim 1; SEQ ID NO 267; 458bp + Sequence Listing; English							

XX The invention relates to a secretory polynucleotide (designated spm)
 CC comprising any of 567 polynucleotide sequences (AB235837-AB236403), a
 CC naturally occurring polynucleotide sequence at least 90 % identical to
 CC the polynucleotide sequence, a polynucleotide complementary to them or an
 CC RNA equivalent of them. The polypeptide or polynucleotide are useful for
 CC treating, preventing or diagnosing a disease or condition associated with
 CC the expression of functional SPM. These are particularly useful for
 CC diagnosing, treating or preventing autoimmune/inflammatory disorders
 CC (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's
 CC disease), neurological disorders (e.g. epilepsy, Huntington's disease,
 CC dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,
 CC multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety,
 CC schizophrenia or amnesia), or cell proliferative disorders (e.g.
 CC psoriasis, polycythemia vera, or cancers including adenocarcinoma,
 CC leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain,
 CC breast, cervix or prostate).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

Sequence 1334 BP; 299 A; 381 C; 394 G; 260 T; 0 other;

Query Match 56.7%; Score 749; DB 25; Length 1334;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 799; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 522 CGAGAGTGGAGTTGTTTCATGATCATCATGTTGGTGTGATGATGTTGGTGGT 581
DB 105 CGGAGCTGGAGTTGTTTCATGATCATCATGTTGGTGTGATGATGTTGGTGGT 164
OY 582 TGATCAGCTGCTCTGAGCCAGTACAGCTGTCTGACGGTCTTCATCAGCCGCA 641
DB 165 TGATCAGCTGCTCTGAGCCAGTACAGCTGTCTGACGGTCTTCATCAGCCGCA 224
OY 642 GCCAGGGGGGAGAGAGAAGATGCTCTCAGAGAGATGCTGGGCTTCGAGCA 701
DB 225 GCCAGGGGGGAGAGAGAAGATGCTCTCAGAGAGATGCTGGGCTTCGAGCA 284
OY 702 GCACAGTGTACAGCAACGGAATCCAGAGCCGAGTGTACGCCCGCTGGCCACAG 761
DB 285 GCACAGTGTACAGCAACGGAATCCAGAGCCGAGTGTACGCCCGCTGGCCACAG 344
OY 762 ACCGCTGGGCGCTGCGCCCTTCGCCAGCGGAGCGCTTCACCGCTTCAGCCACT 821
DB 345 ACCGCTGGGCGCTGCGCCCTTCGCCAGCGGAGCGCTTCACCGCTTCAGCCACT 404
OY 822 ATCCGTACCTGACAGACAGATCCAGCTGCCACCCACCATCTCGCTGCAGACGGGAGG 881
DB 405 ATCCGTACCTGACAGACAGATCCAGCTGCCACCCACCATCTCGCTGCAGACGGGAGG 464
OY 882 AGCCCCACCTTACACAGGGGCCCTTCACACCTTCGGGAGCCCGAGCAGCAGCTGG 941
DB 465 AGCCCCACCTTACACAGGGGCCCTTCACACCTTCGGGAGCCCGAGCAGCAGCTGG 524
OY 942 AACTGAACCGGAGAGTGGTGGCGCAGCCCAAAACAGAACCATCTTCAGACGTGACATGA 1001
DB 525 AACTGAACCGGAGAGTGGTGGCGCAGCCCAAAACAGAACCATCTTCAGACGTGACATGA 584
OY 1002 TGGATAGTGCAGAGTGGGCGGCGCTTCGCCAGAGATTAACCTGGGGCATACGCCCA 1061
DB 585 TGGATAGTGCAGAGTGGGCGGCGCTTCGCCAGAGATTAACCTGGGGCATACGCCCA 644
OY 1062 CGTGTACGAGCAGCGGGGCGCATGAGAGGGCGCCGCCCACTACAGCGAGTCAATCG 1121
DB 645 CGTGTACGAGCAGCGGGGCGCATGAGAGGGCGCCGCCCACTACAGCGAGTCAATCG 704
OY 1122 GCCACTACCCGGGGGTCTCTTCCAGACACAGCAGAGAGAGTGGCGCCCTCTCTTGG 1181
DB 705 GCCACTACCCGGGGGTCTCTTCCAGACACAGCAGAGAGAGTGGCGCCCTCTCTTGG 764
OY 1182 AGGGAGCCCGGTCTCCACACACACATCGGCGCCCTAGAGAGCCGACCATCTGGAGCA 1241

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DB 765 AGGGAGCCCGGCTCCACCACACACATCGGCCCTAGAGAGCGCAGCCATCTGGAGCA 824
OY 1242 AAGAGAAGGATTAACAGAAAGACACCTCTCTAGAGGTCCCGAGGGGCGCGCTGGG 1301
DB 825 AAGAGAAGGATTAACAGAAAGACACCTCTCTAGAGGTCCCGAGGGGCGCGCTGGG 884
OY 1302 CTGCGTAGTGAAGAAAGCGAG 1321
DB 885 CTGCGTAGTGAAGAAAGCGAG 904

RESULT 7
AAA75163
ID AAA75163 standard; cDNA; 969 BP.
AC AAA75163;
XX
DT 15-JAN-2001 (first entry)
XX
DE cDNA clone encoding a human TANGO 261 polypeptide.
XX
KM TANGO 266; TANGO 216.; TANGO 261; TANGO 267;
KM cellular proliferation; cellular differentiation; cellular adhesion;
KM von Willebrand factor-associated disorder; cell trafficking; cancer;
KM hematopoietic associated disease; atelectasis; pulmonary congestion;
KM oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
KM intestinal disorder; spleen associated disease; renal disorder;
KM cardiovascular disorder; ischemic heart disease; hydrocephalus;
KM brain herniation; latrogenic disease; inflammation; meningitis;
KM Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;
KM multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
XX
OS Homo sapiens.
FH
FT Key Location/Qualifiers
FT CDS 6..764
FT /tag= a
FT /product= "TANGO 261"
PD
XX WO200052022-A1.
XX
XX 08-SEP-2000.
XX
XX 01-MAR-2000; 2000WO-US05226.
XX
XX 01-MAR-1999; 99US-0122458.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Barnes TM, Holtzman DA, Sharp JD, Fraser CC;
XX
XX WPI: 2000-579269/54.
XX
XX P-PSDB: AMB18461.
XX
XX Novel human and murine secreted proteins designated TANGO 216, 261,
XX 262, 266 and 267 useful as modulating agents of cellular processes,
XX e.g. for treating cancer -
XX
XX Disclosure: Page -: 175pp; English.
XX
XX AAA75163-65 encode human TANGO 261 proteins. The specification also
XX describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO
XX polypeptides can be used to modulate cellular proliferation, modulate
XX cellular differentiation and/or modulate cellular adhesion. The
XX proteins can be used to treat any von Willebrand factor-associated
XX disorder, regulate extracellular matrix structuring, cellular adhesion,
XX and cell trafficking and/or migration, modulate cellular interactions,
XX modulate cell adhesion in proliferative disorders, such as cancer,
XX modulate the proliferation, differentiation, and/or function of cells
XX that appear in the bone marrow, and leukocytes, treat bone marrow, blood
XX and hematopoietic associated diseases and disorders, atelectasis,
XX pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial
XX asthma and bronchiectasis, intestinal disorders, spleen associated

```

Db 795 TAGGTGAAAGGCAG 809

CC hydrocephalus and e

hydrocephalus and encephalitis, and treat hepatic disorders.

QY 1090 GGGGCCCCCCCCCTACAGGAGGTCATGCGCCACTACCGGGGTCCTCTCCAGCA 1149
 DB 1187 GGGGCGCGCGCCCTACAGGAGGTCATGCGCCACTACCGGGGTCCTCTCCAGCA 1246
 QY 1150 CCAGAGAGCACTGGGCGCGCCCTCTCTGAGAGGAGCCCGGCTCCACACACACT 1209
 DB 1247 CCAGAGAGCACTGGGCGCGCCCTCTCTGAGAGGAGCCCGGCTCCACACACACT 1306
 QY 1210 GCGGCCCCCTAGAGAGCGAGCATCTGAGAGCAAGAGATTAACAGAAAGAGACACC 1269
 DB 1307 GCGGCCCCCTAGAGAGCGAGCATCTGAGAGCAAGAGATTAACAGAAAGAGACACC 1366
 QY 1270 TCTTAGGTCCTCCAGGGG 1289
 DB 1367 TCTTAGGTCCTCCAGGGG 1386

RESULT 11
 AAF65983 standard; cDNA; 408 BP.
 AAF65983;
 AAF65983;
 09-APR-2001 (first entry)
 Novel human polynucleotide, SEQ ID NO: 1739.
 Human; cytosolic; gene therapy; colon cancer; prostate cancer;
 breast cancer; lung cancer; cancer detection; ss.
 Homo sapiens.
 WO200102568-A2.
 11-JAN-2001.
 30-JUN-2000; 2000MO-US18374.
 02-JUL-1999; 99US-0142310.
 PR 02-JUL-1999; 99US-0142311.
 XX
 XX (CHIR) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.
 XX Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J, Kassam A;
 PI Reinhard C, Randazzo F, Kennedy GC, Pot D, Lamson G, Drmanac R;
 PI Cirenjakov R, Drmanac S, Dickson M, Labat I, Leshowitz D;
 PI Kita D, Garcia V, Jones LM, Strache-Crain B;
 WPI: 2001-091805/10.

Library of polynucleotides for diagnosing a cancerous state of a mammalian cell and detecting cancer, particularly of the colon or prostate, comprises 3351 human polynucleotide sequences -

Claim 9; Page 793; 1046bp; English.

The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polynucleotides and their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and preventive interventions. The polynucleotides, polypeptides and antibodies against them can be used in pharmaceutical compositions to treat the cancers and proliferative disorders such as neoplasia, dysplasia and hyperplasia.

XX SQ Sequence 408 BP; 81 A; 159 C; 115 G; 53 T; 0 other;
 Query Match 30.4%; Score 401; DB 22; Length 408;
 Best Local Similarity 100.0%; Pred. No. 4, 1e-170;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 583 GATCAGTGCCTGCTGAGCAGCTACAGAGTGTCTGACAGGTCCTCATCAGCGGACAG 642
 DB 8 GATCAGTGCCTGCTGAGCAGCTACAGAGTGTCTGACAGGTCCTCATCAGCGGACAG 67
 QY 643 CCAGGGGCGGAGAGAGAGATGCTCTGTCTCAGAGAGATGCTGTGGCCTCGAGAG 702
 DB 68 CCAGGGGCGGAGAGAGAGATGCTCTGTCTCAGAGAGATGCTGTGGCCTCGAGAG 127
 QY 703 CACAGTGTGAGGCAACAGAGATCCAGAGGCGGAGGTCCTGAGGCGGCGGCGGACCGA 762
 DB 128 CACAGTGTGAGGCAACAGAGATCCAGAGGCGGAGGTCCTGAGGCGGCGGCGGACCGA 187
 QY 763 CCGCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 822
 DB 188 CCGCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 247
 QY 823 TCCGTACCTGACAGCAGAGATGAGCTGCTGACCATCTGCTGTGAGAGGGAGAGA 882
 DB 248 TCCGTACCTGACAGCAGAGATGAGCTGCTGACCATCTGCTGTGAGAGGGAGAGA 307
 QY 883 GCCCCACCTACAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 942
 DB 308 GCCCCACCTACAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 367
 QY 943 ACTGAACCGGAGTGTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 983
 DB 368 ACTGAACCGGAGTGTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 408

RESULT 12
 AAI59654/c
 ID AAI59654 standard; cDNA; 1069 BP.
 XX
 XX AAI59654;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 3643.
 XX
 KW Human; neurotropic; immunosuppressant; cytosolic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW Leukemia; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000MO-US34263.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-APR-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

XX Sequence 474 BP; 62 A; 136 C; 186 G; 90 T; 0 other;
 SO Query Match 27.6%; Score 364; DB 25; Length 474;
 Best Local Similarity 99.8%; Pred. No. 1.7e-153;
 Matches 414; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 714 GCACGAGATCCACAGAGCCGAGGTCTACAGCCCGCTGGCCACAGCCGCTGGCGG 773
 DB 474 GCAACGAGATCCACAGAGCCGAGGTCTACAGCCCGCTGGCCACAGCCGCTGGCGG 415
 OY 774 TGGCGCCCTGGCCAGAGGGAGGCGTTCACCGCTTCACCCATCTGCTACCTGC 833
 DB 414 TGGCGCCCTGGCCAGAGGGAGGCGTTCACCGCTTCACCCATCTGCTACCTGC 355
 OY 834 AGCAGAGATGACCTGGCCACCAACATCTGCTGTAGAGGGAGAGAGCCCACTCT 893
 DB 354 AGCAGAGATGACCTGGCCACCAACATCTGCTGTAGAGGGAGAGAGCCCACTCT 295
 OY 894 ACCAGGGCCCTGCACACCTTCAGCTTGGGAGACCCCGAGCAGCTGGAAGTGAACCGG 953
 DB 294 ACCAGGGCCCTGCACACCTTCAGCTTGGGAGACCCCGAGCAGCTGGAAGTGAACCGG 235
 OY 954 AGTGGTGGCGGCGACCCCAACAGAACATCTTCAGAGTACCTGATGATAGTGCA 1013
 DB 234 AGTGGTGGCGGCGACCCCAACAGAACATCTTCAGAGTACCTGATGATAGTGCA 175
 OY 1014 GGGTGGGGGGCCCTGGCCCGCCAGAGTAACTGGGGCATGAGCGCACGTACGGCA 1073
 DB 174 GGGTGGGGGGCCCTGGCCCGCCAGAGTAACTGGGGCATGAGCGCACGTACGGCA 115
 OY 1074 GCGGCGGGGCGATGAGAGGGCGCGCCGACCTACAGGAGGTATCGGGCACTA 1128
 DB 114 GCGGCGGGGCGATGAGAGGGCGCGCCGACCTACAGGAGGTATCGGGCACTA 60

RESULT 14
 ABR12143/c
 ID ABR12143 standard; cDNA; 693 BP.
 ABR12143;
 05-JUN-2002 (first entry)
 Human MIVR-1 homologous sequence #1.
 Human MIVR-1; Mechanically Induced Vascular Receptor 1;
 cytosolic; cardiant; cerebroprotective; antiarteriosclerotic;
 cardiac cell; anti-apoptotic; vascular endothelial cell;
 cardiac hypertrophy; myocardial infarction; stroke; arteriosclerosis;
 heart failure; A1761441.1.
 Homo sapiens.
 WO200216416-A2.
 28-FEB-2002.
 21-AUG-2001; 2001WO-US26089.
 22-AUG-2000; 2000US-227159P.
 (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 (PFIZ) PFIZER INC.
 Lee RT, Landschulz KT, Kennedy SP, Thompson JF, Turi TG;
 WPI: 2002-280912/32.
 Novel nucleic acid molecule encoding Mechanically Induced Vascular
 Receptor-1 polypeptide, useful for treating cardiovascular diseases
 Disclosure; Page 101; 105pp; English.

XX The invention relates to an isolated nucleic acid molecule encoding a
 CC Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having
 CC cardiac cell anti-apoptotic activity and fragments of it provided
 CC they are not identical to Genbank sequences A1761441.1, A1594390,
 CC NM_004338 and A0177461. Also included are expression vectors, host
 CC cells, the MIVR-1 polypeptide, MIVR-1 binding peptides, modulators of
 CC MIVR-1, contacting a molecule having cardiac cell anti-apoptotic activity
 CC with a candidate agent, where the molecule is a nucleic acid molecule
 CC comprising MIVR-1, IEX-1, VDP-1, Brg-2 and TIS-11d or its
 CC expression product, determining if the anti-apoptotic activity is
 CC modulated and thereby identifying a modulator. The cardiac cell anti-
 CC apoptotic molecules and nucleic acids of the invention are useful for
 CC treating, diagnosing and monitoring progression of such diseases and
 CC disorders as characterized by increased apoptotic cell-death of vascular
 CC endothelial cells e.g. cardiac hypertrophy, myocardial infarction,
 CC stroke, arteriosclerosis and heart failure. The present sequence
 CC is one of the four Genbank sequences (A1761441.1) which are homologous to
 CC the cDNA for human MIVR-1 and which are specifically disclaimed.

SO Sequence 693 BP; 101 A; 205 C; 237 G; 149 T; 1 other;
 Query Match 22.9%; Score 302; DB 24; Length 693;
 Best Local Similarity 100.0%; Pred. No. 1.2e-125;
 Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 885 CCCACCTTACAGAGGCGCCCTGCACCTTCAGCTTGGGACCCGAGCAGAGCTGAAC 944
 DB 587 CCCACCTTACAGAGGCGCCCTGCACCTTCAGCTTGGGACCCGAGCAGAGCTGAAC 528
 OY 945 TGAACCGGAGTGGTGGCGGACCCCAACAGAACATCTTCAGAGTGAACCTGATGG 1004
 DB 527 TGAACCGGAGTGGTGGCGGACCCCAACAGAACATCTTCAGAGTGAACCTGATGG 468
 OY 1005 ATAGTGGAGGTGGGGGCGCCCTGGCCCGCCAGAGTAACTGGGGCATGAGCGCACT 1064
 DB 467 ATAGTGGAGGTGGGGGCGCCCTGGCCCGCCAGAGTAACTGGGGCATGAGCGCACT 408
 OY 1065 GCTACGAGCAGGCGGCGGCGATGAGAGGGCGCGCCGACCTACAGAGGTGATCGGCC 1124
 DB 407 GCTACGAGCAGGCGGCGGCGATGAGAGGGCGCGCCGACCTACAGAGGTGATCGGCC 348
 OY 1125 ACTACCGGGGCTCTCTTCCAGACACAGCAGAGCATGGGCGCCCTTGTGTGAGG 1184
 DB 347 ACTACCGGGGCTCTCTTCCAGACACAGCAGAGCATGGGCGCCCTTGTGTGAGG 288
 OY 1185 GG 1186
 DB 287 GG 286

RESULT 15
 AA252964
 ID AA252964 standard; cDNA; 812 BP.
 AA252964;
 14-MAR-2000 (first entry)
 Human prostate tumor cDNA library derived EST fragment #107.
 Human prostate tumor cDNA library derived EST fragment #107.
 Pancreas; tumor; EST; expressed sequence tag; human; cytosolic;
 treatment; ds.
 Homo sapiens.
 DEL19820190-A1.
 04-NOV-1999.
 28-APR-1998; 98DE-1020190.
 28-APR-1998; 98DE-1020190.

GenCore version 5.1.6
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OW nucleic - nucleic search, using sw model

Run on: August 27, 2003, 21:24:48 ; Search time 3109 Seconds

(without alignments)
10326.862 Million cell updates/sec

Title: US-09-934-249-1

Perfect score: 1321

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Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 44005525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:
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2: em_esthum:*
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8: em_hic:*
9: gb_est1:*
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11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_huv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_fod:*
26: em_gss_phg:*
27: em_gss_vrt:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1.	632	47.8	1046	12	BM922276 AGENCOURT
2	614	46.5	967	13	BM641849 AGENCOURT
3	568	43.0	916	13	BM954555 AGENCOURT
4	558	42.2	609	13	BM636742 hdl3h06.y

5	550	41.6	551	12	BM141979
6	533	40.3	951	12	AL558881
7	518	39.2	729	13	BM575741
8	511	38.7	850	13	BM602918
9	497	37.6	890	13	BM690750
10	471	35.7	1068	13	BM527705
11	468	35.4	655	13	BM691705
12	450	34.1	964	13	BM859860
13	449	34.0	945	13	BM539219
14	445	33.7	782	12	BM015170
15	442	33.5	602	14	CA431191
16	441	33.4	461	12	BM712680
17	437	33.1	633	12	BM714472
18	428	32.4	588	13	BM624784
19	425	32.2	1007	9	AL558882
20	424	32.1	1201	9	AL517150
21	422	31.9	844	13	BM686793
22	422	31.9	938	13	BM157842
23	422	31.9	952	13	BM157959
24	422	31.9	1280	13	BM691500
25	417	31.6	559	10	BE855409
26	417	31.6	629	13	BM730650
27	406	30.7	1400	12	BM559329
28	401	30.4	730	12	BM677602
29	399	30.2	626	12	BM974296
30	393	29.8	728	13	BM683523
31	390	29.5	973	13	BM169156
32	383	29.0	570	13	BM575582
33	377	28.5	563	12	CB048800
34	365	27.6	552	12	BM713900
35	358	27.1	1127	13	BM174654
36	348	26.3	646	13	BM859841
37	338	25.6	874	13	BM362396
38	331	25.1	899	13	BM196912
39	327	24.8	547	12	BM676516
40	324	24.5	613	10	BM680325
41	302	22.9	651	14	CB554226
42	302	22.9	593	9	AI761441
43	291	22.0	502	291	AI921394
44	288	21.8	668	14	CB044866
45	286	21.7	446	12	BM681946

ALIGNMENTS

RESULT 1
BM922276
LOCUS AGENCOURT_6707077 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5754437
DEFINITION 5', mRNA sequence.
ACCESSION BM922276
VERSION BM922276.1 GI:19372655
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1046)
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaphs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: L1AM12791 row: n column: 06
High quality sequence stop: 671.

Db	Accession	Source	Organism	Reference	Authors	Title	Journal	Comment
Db	241	CGCCTGGGCGCGCGCCCTTGGCCACGAGGAGCGGTCCACCGCTTCCACCCACCTAT						
Qy	824	CCGACCTGGACGACAGATGAGACTGTGCACCCACACATCTGTGTGTAGAGAGGAGAG						
Db	301	CCGTACCTGGACGACAGATGAGACTGTGCACCCACACATCTGTGTGTAGAGAGGAGAG						
Qy	884	CCCCACCCCTTACGACGAGGCGCCCTTGACACCTCCAGCTTGGGAGACCCCGAGACACTGGAA						
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Qy	944	CTGAACCGGGAGTGGGTGCGCGACACCCCAACAGAACCATCTTGTGACAGTGCCTGATG						
Db	421	CTGAACCGGGAGTGGGTGCGCGACACCCCAACAGAACCATCTTGTGACAGTGCCTGATG						
Qy	1004	GATAGTGCACAGGTGGGCGGCGCCCTTGACACCTCCAGCACTGTGAGGAGATGAGCGACG						
Db	481	GATAGTGCACAGGTGGGCGGCGCCCTTGACACCTCCAGCACTGTGAGGAGATGAGCGACG						
Qy	1064	TGCTACGCGACGCGGCGGCGGCGATGAGGAGGCGCGCGCCACCTACAGGAGGTATCGGC						
Db	541	TGCTACGCGACGCGGCGGCGGCGATGAGGAGGCGCGCGCCACCTACAGGAGGTATCGGC						
Qy	1124	CACACACCGGGGCTCTCTCTTCCACACACAGACAGAGTGGGCGCGCTCTCTCTGTGAG						
Db	601	CACACACCGGGGCTCTCTCTTCCACACACAGACAGAGTGGGCGCGCTCTCTCTGTGAG						
Qy	1184	GGGACCGCGGCTCCACACACACACATCGCGCCCTAGAGAGCGAGCCATCTGGAG						
Db	661	GGGACCGCGGCTCCACACACACACATCGCGCCCTAGAGAGCGAGCCATCTGGAG						
RESULT 3								
LOCUS	B0954555							
DEFINITION	AGNC00097.8825282							
ACCESSION	B0954555							
VERSION	B0954555.1							
KEYWORDS	EST.							
SOURCE	Homo sapiens (human)							
ORGANISM	Homo sapiens							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.							
TITLE	1 (bases 1 to 916)							
JOURNAL	NIH-MGC http://mgc.ncl.nih.gov/ .							
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)							
	Unpublished							
	Contact: Robert Strausberg, Ph.D.							
	Email: cgapbs-remail.nih.gov							
	Tissue Procurement: Dr. James R. Lupski							
	CDNA Library Preparation: Life Technologies, Inc.							
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)							
	DNA Sequencing by: Agencourt Bioscience Corporation							
	Clone distribution: MGC clone distribution information can be							
	found through the I.M.A.G.E. Consortium/LNLN at:							
	http://image.lnl.gov							
	Plate: L1AM13626 row: c column: 10							
	High quality sequence stop: 669.							
FEATURES								
SOURCE	Location/Qualifiers							
	1..916							

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6204609"
/sex="male"
/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
/clone_lib="lmpski.sciotic.nerve"
/note="vector: pCMV-Sport6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT primers. Directionally cloned using the following adaptors:

```

5'-TACGACCCACGGGCTCG-3' and 5'-ACATGCTTTCATGTCGAGCGGCCCTT(15)-3'. Size selected > 1 kb for average insert length 1.87 kb. This is a primary library, non-amplified, library constructed by Life Technologies and donated by J. Lipski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies.

BASE COUNT	162 a	354 c	273 g	127 t
ORIGIN				

Query Match	Similarity	Score	DB	Length
Best Local Similarity	99.7%	Pred. No. 4.3e-241		
Matches	668	Conservative	0	Mismatches 2; Indels 0; Gaps 0;
QY	344	GCGCCGGCGGAGAGCCCCCGCGCGCCCGCGAGCCCCCGCGCGCCCGCGCGCGCGCC	403	
Db	1	GCGCCGGCGGAGAGCCCCCGCGCGCCCGCGAGCCCCCGCGCGCCCGCGCGCGCGCC	60	
QY	404	GCGCCGTCATATGACACCGCTTGATGGGGTCAACAGACACCGCCGCCGCCGGCGAG	463	
Db	61	GCGCCGTCATATGACACCGCTTGATGGGGTCAACAGACACCGCCGCCGCCGGCGAG	120	
QY	464	CCCAATGCTCTCTGACAGTGTGCACTGGCAAAAGCTCTTGTCTCCAGAGCATGAGATACG	523	
Db	121	CCCAATGCTCTCTGACAGTGTGCACTGGCAAAAGCTCTTGTCTCCAGAGCATGAGATACG	180	
QY	524	GAGCTGGAGTTGTTGTCAGATCATCATCTGTGGTGGATGAGTGGATGGTGGTGGT	583	
Db	181	GAGCTGGAGTTGTTGTCAGATCATCATCTGTGGTGGATGAGTGGATGGTGGTGGT	240	
QY	584	ATCACGTGCTCTGTCGACCTACAGCTGTCTGACAGGTCCTTCATACGCCGACAGC	643	
Db	241	ATCACGTGCTCTGTCGACCTACAGCTGTCTGACAGGTCCTTCATACGCCGACAGC	300	
QY	644	CAGGGGGGAGAGAGAGAAATGCCCTGCTCAGAAAGATGCTGTGGGCCCTCGGAGAGC	703	
Db	301	CAGGGGGGAGAGAGAGAAATGCCCTGCTCAGAAAGATGCTGTGGGCCCTCGGAGAGC	360	
QY	704	ACAGTGTACGAGCAACGAGATCCAGAGCGCAGAGGTCTACGCCCCGCTCGGCGCCAGC	763	
Db	361	ACAGTGTACGAGCAACGAGATCCAGAGCGCAGAGGTCTACGCCCCGCTCGGCGCCAGC	420	
QY	764	CGCCTGGCCGTGCGGCCCTTTCGCCACGCGGAGCGCTTTCACCGCTTCAGCCACCTAT	823	
Db	421	CGCCTGGCCGTGCGGCCCTTTCGCCACGCGGAGCGCTTTCACCGCTTCAGCCACCTAT	480	
QY	824	CCGTAACCTGGACAGCAAGATAGACTCTGCACCCACCAATCTGGCTGTAGAGGGGAGAG	883	
Db	481	CCGTAACCTGGACAGCAAGATAGACTCTGCACCCACCAATCTGGCTGTAGAGGGGAGAG	540	
QY	884	CCCCCACCCTTACAGAGGGGCCCTTGACACCTTCAGCTTGGGAGCCCGAGCAGACGTGGAA	943	
Db	541	CCCCCACCCTTACAGAGGGGCCCTTGACACCTTCAGCTTGGGAGCCCGAGCAGACGTGGAA	600	
QY	944	CTGAACCGGGAGTGGGTGCGGCAACCCCAAAAGAACCAATCTTCGACAGTGACCTGATG	1003	
Db	601	CTGAACCGGGAGTGGGTGCGGCAACCCCAAAAGAACCAATCTTCGACAGTGACCTGATG	660	
QY	1004	GATAGTGCCA 1013		
Db	661	GATAGTGCCA 670		
RESULT 4	B0636742			
LOCUS	B0636742	609 bp	mRNA	linear
DEFINITION	hd13h06.y1 Human Retina cDNA (Un-normalized, unambigified): hd/he			
ACCESSION	B0636742			
VERSION	B0636742.1	GI:21761201		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			

REFERENCE 1 (bases 1 to 609)
 AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A., Touchman
 TITLE J.M., Bouffard,G., Smith,D. and Peterson,K.
 JOURNAL Mol. Vis. 8 (4), (2002) In press
 COMMENT Section on Molecular Structure and Function
 National Eye Institute
 6/331, NIH, Bethesda, MD 20892-2740, USA
 Tel: 301 402 3452
 Fax: 301 496 0078
 Email: gtaeme@helix.nih.gov
 Plate: 13 row: h column: 06
 Seq primer: M13RP1 reverse primer (AB1).
 Location/Qualifiers

FEATURES
 SOURCE 1..609
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="hd13h06"
 /tissue_type="Retina"
 /dev_stage="Adult"
 /lab_host="EMDH10B"
 /clone_lib="Human Retina cDNA (Un-normalized, unamplified)"
 /note="Organ: Eye; Vector: pSPORT1; Neural retina tissue was dissected from two 80 year old donors with no observed eye disease. 100ug of total RNA was used for library construction. A directionally cloned cDNA library in the pSPORT1 vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the Superscript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adaptor [5'-pGACTAGTTCATGATCGGCGGCC(T)15-3'] primer. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

BASE COUNT 114 a 238 c 182 g 75 t

Query Match 42.2%; Score 558; DB 13; Length 609;
 Best Local Similarity 99.8%; Pred. No. 1.2e-236;
 Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

631 CAGCCGCGACAGCCAGGGGCGGAGAGAGAGATGCTCTCAGACAGATGCTGTG 690
 1 CAGCCGCGACAGCCAGGGGCGGAGAGAGATGCTCTCAGAGATGCTGTG 60
 691 GCCCTCGAGAGACAGTGTGAGGCAAGCAATCCAGAGCGGAGGCTCTGCGCCG 750
 61 GCCCTCGAGAGACAGTGTGAGGCAAGCAATCCAGAGCGGAGGCTCTGCGCCG 120
 751 TCGGCGCCACGACGCGCTGTGCGCCCTTGTGCGCCAGGCGGAGGCTCTCAACG 810
 121 TCGGCGCCACGACGCGCTGTGCGCCCTTGTGCGCCAGGCGGAGGCTCTCAACG 180
 811 CCAGCCCACTATCTGCTGCTGAGAGAGATGAGTGTGCGCCAGCCACTCTGCTTC 870
 181 CCAGCCCACTATCTGCTGCTGAGAGAGATGAGTGTGCGCCAGCCACTCTGCTTC 240
 871 AGAGGGGAG 930
 241 AGAGGGGAG 300
 931 GCAGAGCTGGAAGTGAACCGGAGTGGTGGCGGCGACCCCAACAGAACATCTTGA 990
 301 GCAGAGCTGGAAGTGAACCGGAGTGGTGGCGGCGACCCCAACAGAACATCTTGA 360

OY 991 CAGTGAAGTATGATGATAGTCCAGGCTGGGCGGCGCCCTGCCCCCAGACAGTAACTCGGG 1050
 361 CAGTGAAGTATGATGATAGTCCAGGCTGGGCGGCGCCCTGCCCCCAGACAGTAACTCGGG 420
 OY 1051 CATCAGCGCCACGCTGTCTAGCGGAGCGGCGGCGGCGCATGAGAGGCGCGCCGACCTAGC 1110
 421 CATCAGCGCCACGCTGTCTAGCGGAGCGGCGGCGGCGCATGAGAGGCGCGCCGACCTAGC 480
 OY 1111 CGAGGTATGATGATGATAGTCCAGGCTGGGCGGCGCCCTGCCCCCAGACAGTAACTCGGG 1170
 481 CGAGGTATGATGATGATAGTCCAGGCTGGGCGGCGCCCTGCCCCCAGACAGTAACTCGGG 540
 OY 1171 CTCCTGCTGAGAGGAGGAGCGGCTCCACACACACATCGCGCCCTAGAGAGCGCAGC 1230
 541 CTCCTGCTGAGAGGAGGAGCGGCTCCACACACACATCGCGCCCTAGAGAGCGCAGC 600
 OY 1231 CATCTGGAG 1239
 601 CATCTGGAG 609

RESULT 5
 BM141979
 LOCUS 551 bp mRNA linear EST 12-MAR-2002
 DEFINITION 1125a11.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
 cDNA clone IMAGE:5677341 5' similar to TR:09JUD3 Q9JUD3 D71847.1
 ; mRNA sequence.

ACCESSION BM141979.1 GI:17152046
 VERSION BM141979
 KEYWORDS EST.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 551)
 AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
 Lemishka,I., Secaer,M., Brestelli,J., Gradwohl,G., Clifton,S.,
 Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
 Schmitt,A., Theising,B., Ritzer,E., Ronko,I., Bennett,J., Cardenas
 , M., Gibson,M., McCann,R., Cole,R., Tsagarisvill,I., Williams,T.,
 Jackson,Y. and Bowers,Y.
 Endocrine Pancreas Consortium

TITLE Unpublished
 JOURNAL Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 COMMENT Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept. of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@iuhp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Juliana Brown
 (brown@fas.harvard.edu) This sequence now available from the IMAGE
 consortium, for clone orders contact: info@image.llnl.gov
 Seq primer: -40RP from GIDCO
 High quality sequence stop: 429.
 Location/Qualifiers

FEATURES
 source 1..551

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5677341"
 /sex="Both"
 /tissue_type="Islets of Langerhans"
 /dev_stage="Adult"
 /lab_host="DH10B"
 /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
 /note="Organ: Pancreas; Vector: pSPORT1; Site: 1; Not 1;
 Site 2: Sal 1; Starting library constructed using
 Superscript Plasmid Library kit (Life Technologies). cDNA
 made by oligo-dT priming. Size-selected by column

fractionation: average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806: 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."

BASE COUNT 110 a 218 c 157 g 66 t

Query Match 41.6%; Score 550; DB 12; Length 551;
Best Local Similarity 100.0%; Pred. No. 4.3e-233;

Matches 550; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 714 GCACGGAATCCAGAGCCGCGAGCTTACGCCCCCGCTGCGCCACCGCCCTGGCCG 773
1 GCACGGAATCCAGAGCCGCGAGCTTACGCCCCCGCTGCGCCACCGCCCTGGCCG 60
774 TGCCGCTTGGCCGAGGCGGAGGCTTCCACCGCTTCCAGCCACCTATCCGTACGTC 833
61 TGCCGCTTGGCCGAGGCGGAGGCTTCCACCGCTTCCAGCCACCTATCCGTACGTC 120
DB 834 AGCAGAGATGAGCTGCGACCCACCATCTGCTGTAGACGGGAGAGCCCGACCCCT 893
121 AGCAGAGATGAGCTGCGACCCACCATCTGCTGTAGACGGGAGAGCCCGACCCCT 180
DB 894 ACCAGGGCCCTGACACCTCCAGCTTGGGAGCCCGAGCAGAGCTGTGAATGAACCGG 953
181 ACCAGGGCCCTGACACCTCCAGCTTGGGAGCCCGAGCAGAGCTGTGAATGAACCGG 240
DB 954 AGTCGCTGCGGACCCCAAGAGACATCTTGCAGAGTGTGATGATGATGCA 1013
241 AGTCGCTGCGGACCCCAAGAGACATCTTGCAGAGTGTGATGATGATGATGCA 300
DB 1014 GCGTGGGCGCCCTGCCCCCGCCAGCACTGCGGGCATGCGCCACGTCGTAAGCA 1073
301 GCGTGGGCGCCCTGCCCCCGCCAGCACTGCGGGCATGCGCCACGTCGTAAGCA 360
DB 1074 GCGGCGGCGCATGAGAGGGGCGCGCCCACTTAAGAGAGTATCGGCCACTACCGG 1133
361 GCGGCGGCGCATGAGAGGGGCGCGCCCACTTAAGAGAGTATCGGCCACTACCGG 420
DB 1134 GGTCTCTCTTCCAGACACGACAGAGAGTGGGCGCCCTCTTGTGGAGGGGAGCCG 1193
421 GGTCTCTCTTCCAGACACGACAGAGAGTGGGCGCCCTCTTGTGGAGGGGAGCCG 480
DB 1194 TCACACACACACATCGGCGCCCTAGAGAGCGCAGCATCTGAGCAAGAGAGATA 1253
481 TCACACACACACATCGGCGCCCTAGAGAGCGCAGCATCTGAGCAAGAGAGATA 540
DB 1254 AACAGAAAGG 1263
541 AACAGAAAGG 550

RESULT 6

AL558881 951 bp mRNA linear EST 31-MAY-2003

LOCUS AL558881 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED

DEFINITION Homo sapiens cDNA clone CSODJ015YF12 3-PRIME, mRNA sequence.

ACCESSION AL558881

VERSION AL558881.2 GI:31283014

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 951)

AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished
COMMENT On Feb 15, 2001 this sequence version replaced gi:12903836.

CONTACT Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France

Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
9945.r for more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODJ015DC06NP1&cluster=9945.r. Contact :
Feng Liang Email: fliang@life.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Fareday Avenue Genoscope sequence ID : CSODJ015DC06NP1.

FEATURES

source 1. 951
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODJ015YF12"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/clone_11b="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 141 a 275 c 318 g 201 t 16 others

Query Match 40.3%; Score 533; DB 9; Length 951;

Best Local Similarity 99.5%; Pred. No. 1.4e-225;

Matches 733; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

DB 585 TCAGTGCCTGCTGAGCCACTTACAGCTGTCTGACAGGCTCTTCAATACGGCGACAGC 644
846 TCAGTGCCTGCTGAGCCACTTACAGCTGTCTGACAGGCTCTTCAATACGGCGACAGC 787
DB 645 AGGCGGAGAGAGAGAGAGTGCCTGTCTGAGAGAGAGTGCCTGTGGCGCCGGAGAGA 704
786 AGGCGGAGAGAGAGAGAGTGCCTGTCTGAGAGAGAGTGCCTGTGGCGCCGGAGAGA 727
DB 705 CAGTGTACAGGCAAGAGATCCAGAGCCGAGGTACGCGCCGCTCGGCCACCGAC 764
726 CAGTGTACAGGCAAGAGATCCAGAGCCGAGGTACGCGCCGCTCGGCCACCGAC 667
DB 765 GCGTGGCGGCGCCCTTGCAGCGGAGCGCTTCCAGCGCTTCCAGCGCCACTATC 824
666 GCGTGGCGGCGCCCTTGCAGCGGAGCGCTTCCAGCGCTTCCAGCGCCACTATC 607
DB 825 CGTACCTGAGACAGAGATGAGACGCGCCACCAACCATCTGCTGACAGAGGGAGAGAG 884
606 CGTACCTGAGACAGAGATGAGACGCGCCACCAACCATCTGCTGACAGAGGGAGAGAG 547
DB 885 CCCACACCTTACAGAGGCGCCCTGACACCTTCTGAGAGCCCGAGAGAGCTGAGAG 944
546 CCCACACCTTACAGAGGCGCCCTGACACCTTCTGAGAGCCCGAGAGAGCTGAGAG 487
DB 945 TGAACCGGAGTGTGGCGGACCCCAAGAGAGATCTTGCAGAGTGAAGCTGATG 1004
486 TGAACCGGAGTGTGGCGGACCCCAAGAGAGATCTTGCAGAGTGAAGCTGATG 427
DB 1005 ATAGTGCAGAGCGTGGGCGGCGCCCTGCGCCCAAGAGAGTGAAGCTGAGAGAG 1064
426 ATAGTGCAGAGCGTGGGCGGCGCCCTGCGCCCAAGAGAGTGAAGCTGAGAGAG 367
DB 1065 GCTACGAGAGCGGCGGCGCATGAGAGGGCGCCCGCCACTTACAGAGAGGATCATG 1124
366 GCTACGAGAGCGGCGGCGCATGAGAGGGCGCCCGCCACTTACAGAGAGGATCATG 307
DB 1125 ACTACCGGGGCTCTCTTCCAGACACAGAGAGAGTGGGCGCCCTCTCTGAGAG 1184
|||||

Db 306 ACTACCGGGGCTCTCTCCAGACACAGACAGTGGGCGCCCTCTCTCTCTGAGG 247
QY 1185 GAGACGGGCTCCACACACACATGCGCCCTTAGAGAGCGGACATCTGGAGCAAG 1244
Db 246 GAGACGGGCTCCACACACACATGCGCCCTTAGAGAGCGGACATCTGGAGCAAG 187
QY 1245 AGAAGGATTAACAGAAAGACACCCCTCTCTAGGTCGCCAGGGGGCGGGCTGGGGCAG 1304
Db 186 AGAAGGATTAACAGAAAGACACCCCTCTCTAGGTCGCCAGGGGGCGGGCTGGGGCAG 127
QY 1305 CGTAGGTGAAGAGCAG 1321
Db 126 CGTAGGTGAAGAGCAG 110

RESULT 7
B0575741/c 729 bp mRNA linear EST 19-JUN-2002
LOCUS UT-H-E21-dbg-h-14-0-UT.s1 NCI CGAP Ch2 Homo sapiens cDNA clone
DEFINITION UT-H-E21-dbg-h-14-0-UT 3', mRNA sequence.
B0575741
B0575741 GI:21479058
EST.

SESSION
KEYWORDS
ORGANISM Homo sapiens (human)
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 729)
NCI CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
Orthopedics

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@iowa.edu
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
Source location/Qualifiers

1..729
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UT-H-E21-dbg-h-14-0-UT"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_id="NCI CGAP Ch2"
/note="Organ: Left Pelvis; Vector: pRT3-Pac (Pharmacia)
With a modified polylinker. Site_1: EcoR I, Site_2: Not I.
NCI CGAP Ch2 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma Grade II. The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pRT3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(d)18 tail. The sequence tag for this library is
TGATACGCT
TAG_LIB-UT-H-E21
TAG_TISSUE-grade-2-chondrosarcoma
TAG_SEQ-ATCAATATG"

BASE COUNT 101 a 213 c 253 g 162 t
ORIGIN

Query Match 39.2%; Score 518; DB 13; Length 729;
Best Local Similarity 99.8%; Pred. No. 6,6e-219;
Matches 368; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 753 GGGCCACGACGCGCTGGCGCTGCGCCCTTGGCCAGCGGAGCGCTTCCACCGCTTCC 812
Db 729 GGGCCACGACGCGCTGGCGCTGCGCCCTTGGCCAGCGGAGCGCTTCCACCGCTTCC 670
QY 813 AGCCCACTATCCGATACCTGACGACGAGATGACCTGACACCCACATCTGCTGTAG 872
Db 669 AGCCCACTATCCGATACCTGACGACGAGATGACCTGACACCCACATCTGCTGTAG 610
QY 873 ACGGGAGAGAGCCGCCACCTACGAGGGCCCTGACACCTCCAGCTTGGGAGCCCGAGC 932
Db 609 ACGGGAGAGAGCCGCCACCTACGAGGGCCCTGACACCTCCAGCTTGGGAGCCCGAGC 550
QY 933 AGCAGCTGACACTGAACCGGAGTGGTCCGGGACCCCAACAGAACATCTTGGACA 992
Db 549 AGCAGCTGACACTGAACCGGAGTGGTCCGGGACCCCAACAGAACATCTTGGACA 490
QY 993 GTGACCTGATGATAGTGGCAGGCTGGGCGCCCTGCGCCCGCCAGAGTAATCTGGGCA 1052
Db 489 GTGACCTGATGATAGTGGCAGGCTGGGCGCCCTGCGCCCGCCAGAGTAATCTGGGCA 430
QY 1053 TCAGCGCCACGTCCTACGCGGCGGCGCGCATGGAGGGGCCGCCACCTACAGCG 1112
Db 429 TCAGCGCCACGTCCTACGCGGCGGCGCGCATGGAGGGGCCGCCACCTACAGCG 370
QY 1113 AGGTCAATGGGCACTACCGGGGCTCTCTCTCAGCAGCAGAGACATGGGCGCGCCT 1172
Db 369 AGGTCAATGGGCACTACCGGGGCTCTCTCTCAGCAGCAGAGACATGGGCGCGCCT 310
QY 1173 CCTTGTGAGGAGGACCGGCTCCACACACACATGCGGCCCTTAGAGCGCAGCCA 1232
Db 309 CCTTGTGAGGAGGACCGGCTCCACACACACATGCGGCCCTTAGAGCGCAGCCA 250
QY 1233 TCTGGAGCAAGAGAGGATTAACAGAAAGACACCTCTAGGTTCCAGGGGGGCGC 1292
Db 249 TCTGGAGCAAGAGAGGATTAACAGAAAGACACCTCTAGGTTCCAGGGGGGCGC 190
QY 1293 GGGCTGGGCGCTGCTAGGTGAAGAGCAG 1321
Db 189 GGGCTGGGCGCTGCTAGGTGAAGAGCAG 161

RESULT 8
B0602918 850 bp mRNA linear EST 20-SEP-2002
LOCUS AGENCOURT.10016502 NIH.MGC.142 Homo sapiens cDNA clone
DEFINITION IMAGE:6497853 5', mRNA sequence.
B0602918
B0602918 GI:23254677
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 850)
NIH-MGC <http://mhc.ncbi.nlm.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: NCI
cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: L10M2679 row: 1 column: 22
High quality sequence stop: 499.

FEATURES

Location/Qualifiers

QY	822	ATTCGTA	CTCTAC	CACAGAT	CAACGTC	GCACCC	ACCACCAT	CTCGTCA	CACAGGGAGG	881
Db	428	ATCGTA <th>CTCTAC</th> <td>CACAGAT</td> <td>CAACGTC</td> <td>GCACCC</td> <td>ACCACCAT <td>CTCGTCA</td> <td>CACAGGGAGG</td> <td>487</td> </td>	CTCTAC	CACAGAT	CAACGTC	GCACCC	ACCACCAT <td>CTCGTCA</td> <td>CACAGGGAGG</td> <td>487</td>	CTCGTCA	CACAGGGAGG	487
QY	882	AGCCCCA <td>CCCTTAC</td> <td>CAAGGG</td> <td>CCCCCTT</td> <td>GCACCTT</td> <td>CCAGCTT</td> <td>CGGAGCC</td> <td>CCGAGCAG</td> <td>AGCTGG</td>	CCCTTAC	CAAGGG	CCCCCTT	GCACCTT	CCAGCTT	CGGAGCC	CCGAGCAG	AGCTGG
Db	488	AGCCCCA <td>CCCTTAC</td> <td>CAAGGG</td> <td>CCCCCTT</td> <td>GCACCTT</td> <td>CCAGCTT</td> <td>CGGAGCC</td> <td>CCGAGCAG</td> <td>AGCTGG</td>	CCCTTAC	CAAGGG	CCCCCTT	GCACCTT	CCAGCTT	CGGAGCC	CCGAGCAG	AGCTGG
QY	942	AAC	TGAAC	CCGGAGT	CGGTGC	GCACAC	CCCCCA	AAGAAC	CAATCTT	CGACAGT
Db	548	AAC	TGAAC	CCGGAGT	CGGTGC	GCACAC	CCCCCA	AAGAAC	CAATCTT	CGACAGT
QY	1002	TGGA	TAGTGC	AGGCTT	GGGGGG	GGCCCC	CTTGC	CCCCC	CCAGCAG	TAGTAC
Db	608	TGGA	TAGTGC	AGGCTT	GGGGGG	GGCCCC	CTTGC	CCCCC	CCAGCAG	TAGTAC
QY	1062	CGGT	CTAC	1069						
	668	CGT	CTAC	675						

RESULT	10
BUS27705	
LOCUS	BUS27705
DEFINITION	BUS27705
ACCESSION	BUS27705
VERSION	BUS27705.1
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	1 (bases 1 to 1068)
AUTHORS	NIH-MGC http://mgc.ncl.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished
COMMENT	Contact: Robert Strausberg, Ph.D.

cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINT)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINT at:
<http://image.llnl.gov>
 Plate: LINC2700 row: k column: 15
 High quality sequence stop: 468.

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6537543"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone.lib="NH_MGC_101"
/note="Organ: Lung; Vector: pOTB7; Site_1: EcoRI; Site_2: XhoI; XhoI: cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using Zap-cDNA Synthesis Kit (Stratagene) and SuperScript II RN (Life Technologies). Note: this is a NIH-MGC Library."

```

BASE COUNT	154 a	445 c	330 g	135 t	4 others
ORIGIN					

Query Match	35.7%;	Score 471;	DB 13;	Length 1068;
Best Local Similarity	100.0%;	Pred. No. 4.5e-198;		
Matches 471;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	92	GGGAAAGCTACGCGAGAGGGCTCAGACCCCGCGGAGAGCGCGGCCCTGGCACCCAT	151
Db	21	GGGAAAGCTAGGCGGACAGAGCTCAGACCCCGCGGAGAGCGCGGCCCTGGCACCCAT	80
QY	152	TTTCCGGAGCGCACCCGCGGGGCTACTGCCGAGCGCCCCGCGGGGCTGGCGAGGGAGCGCGGG	211
Db	81	TTTCCGGAGCGCACCCGCGGGGCTACTGCCGAGCGCCCCGCGGGGCTGGCGAGGGAGCGCGGG	140
QY	212	GGGGGCGCAGCGGAGCGGGCTCCGCGGCACTAGACCCCGCGGCGCCCGCGGGAACTTGGGGG	271
Db	141	GGGGGCGCAGCGGAGCGGGCTCCGCGGCACTAGACCCCGCGGCGCCCGCGGGAACTTGGGGG	200
QY	272	CGACCCGAGCGCGGCGGAGCGCGGGGCGGCTTCCCGCGCGCGCGGCTCTGCATGCGGGG	331
Db	201	CGACCCGAGCGCGGCGGAGCGGGGCGGCTTCCCGCGCGCGCGGCTCTGCATGCGGGG	260
QY	332	CCCCAGCTCGGGGCGCGGGCGGAGACCCCGCGCGCGCCCGCGAGCCCGCGGCCG	391
Db	261	CCCCAGCTCGGGGCGCGGGCGGAGACCCCGCGCGCGCCCGCGAGCCCGCGGCCG	320
QY	392	CGCGCGCGCGCGCGGCGGCTCCATGACCGCGGTTGAGTGGGGGTCAACAGACCGCGCGCG	451
Db	321	CGCGCGCGCGCGCGGCGGCTCCATGACCGCGGTTGAGTGGGGGTCAACAGACCGCGCGCG	380
QY	452	GCGCGCGGGGACCCCAATGTCCTCGACAGTGCACATGCAACAGCTCTTTGTCCAGAGC	511
Db	381	GCGCGCGGGGACCCCAATGTCCTCGACAGTGCACATGCAACAGCTCTTTGTCCAGAGC	440
QY	512	ATGAGAGTCAACGGAGCTGGAGATTGTTCAGATCAATCAATCAATCGTGGTGGTG	562
Db	441	ATGAGAGTCAACGGAGCTGGAGATTGTTCAGATCAATCAATCAATCGTGGTGGTG	491

RESULT 11	
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LOCUS	B0691705 655 bp mRNA linear EST 15-JUL-2002
DEFINITION	AGENCOCURT_8046876 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6208939
ACCESSION	B0691705
VERSION	B0691705.1 GI:21817021
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 655)	NIH-MGC	http://mgc.ncl.nih.gov/	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished
	Contact:	Robert Strausberg, Ph.D.		

CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2367 row: g column: 20
High quality sequence stop: 645.

FEATURES
source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6208939"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="N1H.MGC.110"
/note="Organ: pancreas; Vector: pOTB7; site_1: XhoI;
site_2: EcoRI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCCACGAG(G). Library constructed

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Db	339	ACGGCCGCGGCGTGGCGCCCTTGGCCGAGGGGAGCGCTTCCACGCCCTTCAGGCCACCT	398
QY	822	ATCCGTACTGCAGACAGAGATGACCTGCCACCCACCATCTGCGTCTCAGAGCGGGAGG	881
Db	399	ATCCGTACCTGCAGACAGAGATGACCTGGCACCCACCATCTGCGTCTCAGAGCGGGAGG	458
QY	882	AGCCCCACCCCTACAGAGGCGCCGCGACCCGCCAGCTTCGGGGAGCCCGAGCAGCGCTGG	941
Db	459	AGCCCCACCCCTACAGAGGCGCCCTGCACCTCCAGCTTCGGGAGCCCGAGCAGCGCTGG	518
QY	942	AACCTGAACCGGGAGTCCGTCGCGCGCACCCCAACAGAACCATCTTCGACATGACTGA	1001
Db	519	AACCTGAACCGGGAGTCCGTCGCGCGCACCCCAACAGAACCATCTTCGACATGACTGA	578
QY	1002	TGATTAATGCGCAGGCTGGGCGCGCCCTCGCCCCGACAGTAATTCGGGGCATCAGCGCA	1061
Db	579	TGATTAATGCGCAGGCTGGGCGCGCCCTCGCCCCGACAGTAATTCGGGGCATCAGCGCA	638
QY	1062	CGTACTCAGCGAGCGCGGGCGGCATGTGAGGGGCGCGCCGACACTACAGCAGGTCATCG	1121
Db	639	CGTACTCAGCGAGCGCGGGCGGCATGTGAGGGGCGCGCCGACACTACAGCAGGTCATCG	698
QY	1122	GCCACTACCGGGGCTCTCTCTTCCAGCACACGACAGAGCATGGGGCGCGCCCTCTCTTGGTGG	1181
Db	699	GCCACTACCGGGGCTCTCTCTTCCAGCACACGACAGAGCATGGGGCGCGCCCTCTCTTGGTGG	758
QY	1182	AGGGGACCCGGCTCCACCACACACATCGCGGCCCTTGAAGAGGCGACCATCTGGAGCA	1241
Db	759	AGGGGACCCGGCTCCACCACACACATCGCGGCCCTTGAAGAGGCGACCATCTGGAGCA	818
QY	1242	AAGAGAAAGATTAACAGAAAGAGACCTCTCTCTAGGCTCCCGAGGGGGCGGGGCTGGGG	1301
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QY	1302	CTGCGTAGTGTAAAAAGGCAG 1321	
Db	879	CTGCGTAGTGTAAAAAGGCAG 898	

RESULT 2
 US-09-769-482-2
 Sequence 2, Application US/09769482
 Patent No. 6566130
 GENERAL INFORMATION:
 APPLICANT: SRIVASTAVA, SHIV
 APPLICANT: MOUL, JUDD W.
 APPLICANT: XU, LINDA L.
 APPLICANT: SEGAWA, TAKEHIKO
 TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
 FILE REFERENCE: 04995.0057-00000
 CURRENT APPLICATION NUMBER: US/09/769,482
 CURRENT FILING DATE: 2001-01-26
 PRIOR APPLICATION NUMBER: 60/178,772
 PRIOR FILING DATE: 2000-01-28
 PRIOR APPLICATION NUMBER: 60/179,045
 PRIOR FILING DATE: 2000-01-31
 NUMBER OF SEQ ID NOS: 67
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 2
 LENGTH: 759
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-769-482-2

Query Match	57.2%	Score 755	DB 4	Length 755
Best Local Similarity	100.0%	Pred. No. 1.7e+313		
Matches 755	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	522	CGAGCTGAGTTGTTTCAGATCATCATCTGCTGCTATGATGATGAGGAGCGCG	581
Db	5	CGAGCTGAGTTGTTTCAGATCATCATCTGCTGCTATGATGATGAGGAGGAGCGCG	64

OY	582	TGATACAGTCCGCTCCTAGGCAACATCAACAAGCTGTGTGACGGTCTTATCATAGCCGGACA	644
Db	65	TGATACAGTCCGCTCCTAGGCAACATCAACAAGCTGTGTGACGGTCTTATCATAGCCGGACA	124
OY	642	GCCAGGGGCGAGAGAGAAAGATGCCCTGTCTCAGAAAGATGCTGTGGCCCTCGGAGA	701
Db	125	GCCAGGGGCGAGAGAGAAAGATGCCCTGTCTCAGAAAGATGCTGTGGCCCTCGGAGA	184
OY	702	GCACAGTGTACGGCAAGGAAATCCACAGCCGACGGTCTACGGCCGCGCTCGGCCACG	761
Db	185	GCACAGTGTACGGCAAGGAAATCCACAGCCGACGGTCTACGGCCGCGCTCGGCCACG	244
OY	762	ACCCGCTGGCGCTGCCGCTTTCGCCACAGCGGAGCGGCTTCACCGCTTCAGCCCACT	821
Db	245	ACCCGCTGGCGCTGCCGCTTTCGCCACAGCGGAGCGGCTTCACCGCTTCAGCCCACT	304
OY	822	ATCCGTACTGCACAGCAGAGATTCGACCTGCCACCCACCATCTCGCTGTCAACGGGGAG	881
Db	305	ATCCGTACTGCACACACAGATTCGACCTGCCACCCACCATCTCGCTGTCAACGGGGAG	364
OY	882	AGCCCCACCTTACAGAGGGGCCCTTGCAACCTTCAGCTTCGGGACCCCGAGCAGCACTG	941
Db	365	AGCCCCACCTTACAGAGGGGCCCTTGCAACCTTCAGCTTCGGGAGCCCGAGCAGCACTG	424
OY	942	AACGTAAACGGGAGTCCGTGCGCGCACCCCCAAACAGAACCATCTTGCACAGTAGACCTGA	1001
Db	425	AACGTAAACGGGAGTCCGTGCGCGCACCCCCAAACAGAACCATCTTGCACAGTAGACCTGA	484
OY	1002	TGGATAGTGCAGAGGTGGGGGCCCTTCGCCCCAGCAGTAACTTCGGGCAATCAGCCCA	1061
Db	485	TGGATAGTGCAGAGGTGGGGGCCCTTCGCCCCAGCAGTAACTTCGGGCAATCAGCCCA	544
OY	1062	CGTGTACTAGGCAAGCGGGGCGGCATATGAGAGGGGCGCGCCCACTCAACGCAGAGCTATG	1122
Db	545	CGTGTACTAGGCAAGCGGGGCGGCATATGAGAGGGGCGCGCCCACTCAACGCAGAGCTATG	604
OY	1122	GCCATACCCGGGGGCTCTCTTCCAGACACAGCAGAGTAGTGGGCGGCTCTTGTCTGG	1181
Db	605	GCCATACCCGGGGGCTCTCTTCCAGACACAGCAGAGTAGTGGGCGGCTCTTGTCTGG	664
OY	1182	AGGGAGCCCGGCTCCACACACACACACATCGCGCCCTTAGAGAGCGCAGCATCTGGACCA	1244
Db	665	AGGGAGCCCGGCTCCACACACACACACATCGCGCCCTTAGAGAGCGCAGCATCTGGACCA	724
OY	1242	AAGAGAAGGATTAACAGAAAGGACCCCTCTTAG	1276
Db	725	AAGAGAAGGATTAACAGAAAGGACCCCTCTTAG	759

RESULT 3
 US-09-236-097-7
 Sequence 7, Application US/09236097
 Patent No. 6335165
 GENERAL INFORMATION:
 APPLICANT: -NIR NAVOT ET AL
 TITLE OF INVENTION: METHODS AND KITS FOR CHARACTERIZING GC
 TITLE OF INVENTION: -RICH NUCLEIC ACID SEQUENCES
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
 STREET: 20001 Jefferson Davis Highway, Suite 207
 CITY: Arlington
 STATE: Virginia
 COUNTRY: United States of America
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
 COMPUTER: Twinhead Slimnote-890TX
 OPERATING SYSTEM: MS DOS version 6.2,
 OPERATING SYSTEM: Windows version 3.11
 SOFTWARE: Word for Windows version 2.0 converted to
 SOFTWARE: an ASCII file


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Sequence 1, Application US/07751891B
Patent No. 6180337
GENERAL INFORMATION:
APPLICANT: Caskey, C. T.
Nelson, David L.
Pieretli, Maura
Warren, Stephen T.
Oostra, Ben A.
Fu, Ying-hui
TITLE OF INVENTION: Diagnosis of the Fragile X Syndrome
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas D. Paul
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07751.891B
FILING DATE: 29-Aug-1991
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32, 714
REFERENCE/DOCKET NUMBER: D-5350
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
TELEX: 762829
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3765 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-07-751-891B-1
Query Match
1st Local Similarity 2.1%; Score 28; DB 3; Length 3765;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 56 GCGCGCGCGCGCGCGCGCGCGGAGGCG 83
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DB 44 GCGCGCGCGCGCGCGCGCGCGGAGGCG 71
RESULT 7
US-08-455-073A-1
Sequence 1, Application US/08455073A
Patent No. 5876949
GENERAL INFORMATION:
APPLICANT: Gldeon Dreyfuss
Applicant: Mikiko C. Stoml
APPLICANT: Yan Zhang
TITLE OF INVENTION: Fragile X Related Proteins, Compositions And Methods
TITLE OF INVENTION: Of Making And Using The Same
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5876949-15
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA

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ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,073A
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-2201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4362 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 220..2118
US-08-455-073A-1

Query Match 2.1%; Score 28; DB 2; Length 4362;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 56 GCGCGCGCGCGCGCGCGCGCGCGAGAGCG 83
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Db 68 GCGCGCGCGCGCGCGCGCGCGAGAGCG 95

RESULT 8
US-08-457-273B-41/c
; Sequence 41, Application US/08457273B
; Patent No. 5849995
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael
; APPLICANT: Lin, Biaoyang
; APPLICANT: Nasir, Jamal
; TITLE OF INVENTION: Mouse Model for Huntington's Disease and
; TITLE OF INVENTION: Related DNA Sequences
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Virginia Bennett
; STREET: PO Box 37428
; CITY: Raleigh
; STATE: No. 584995th Carolina
; COUNTRY: US
; ZIP: 27627
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,273B
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Virginia C.
; REGISTRATION NUMBER: 37,092
; REFERENCE/DOCKET NUMBER: 3477-85A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-854-1400
; TELEFAX: 919-854-1401
; INFORMATION FOR SEQ ID NO: 41:

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LOCATION: 316..9748
US-08-246-982A-5

Query Match 2.1%; Score 28; DB 1; Length 10366;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 GAGGAGCGCGCGCGCGCGCGCG 78
DB 469 GAGGAGCGCGCGCGCGCGCGCG 442

RESULT 12
US-08-453-265-5/c
Sequence 5, Application US/08453265
Patent No. 5693757
GENERAL INFORMATION:
APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Guseella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609,3880003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10366 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:
NAME/KEY: CDS
LOCATION: 316..9748
US-08-453-265-5

Query Match 2.1%; Score 28; DB 1; Length 10366;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 GAGGAGCGCGCGCGCGCGCGCG 78
DB 469 GAGGAGCGCGCGCGCGCGCGCG 442

RESULT 13
US-09-325-932A-2/c
Sequence 2, Application US/09325932A
Patent No. 6451604
GENERAL INFORMATION:
APPLICANT: Flynn, Barry
APPLICANT: Lasham, Annette

TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant dev
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 367
TYPE: DNA
ORGANISM: Pinus radiata
US-09-325-932A-2

Query Match 2.0%; Score 26; DB 4; Length 367;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 56 GCGCGCGCGCGCGCGCGCGCGGAG 81
DB 367 GCGCGCGCGCGCGCGCGCGCGGAG 342

RESULT 14
US-09-780-173A-10
Sequence 10, Application US/09780173A
Patent No. 6455307
GENERAL INFORMATION:
APPLICANT: Robert McKay
APPLICANT: Susan M. Freier
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA PRIME EXPRESSION
FILE REFERENCE: RTS-0165
CURRENT APPLICATION NUMBER: US/09/780,173A
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 95
SEQ ID NO 10
LENGTH: 1877
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (344)...(1396)
US-09-780-173A-10

Query Match 2.0%; Score 26; DB 4; Length 1877;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 380 CCGCGCGCGCGCGCGCGCGCGCGC 405
DB 278 CCGCGCGCGCGCGCGCGCGCGCGC 303

RESULT 15
US-08-819-177-2/c
Sequence 2, Application US/08819177
Patent No. 6043083
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Dickens, Martin
TITLE OF INVENTION: INHIBITORS OF THE JNK SIGNAL
TITLE OF INVENTION: TRANSDUCTION PATHWAY AND METHODS OF USE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 27, 2003, 23:06:11 ; Search time 367 Seconds
(without alignments)
8258.053 Million cell updates/sec

Title: US-09-934-249-1

Perfect score: 1321
Sequence: 1 cgaccgcgctcgcgagcga.....ctgcgtagtgtaaaagcag 1321

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1533700 seqs, 1147125425 residues

Hit size : 8

Total number of hits satisfying chosen parameters: 2240168

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA.*

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1229	93.0	4839	12	US-10-241-220-119
3	861	65.2	861	10	US-09-934-249-3
4	800	60.6	1141	12	US-10-301-822-208
5	800	60.6	1141	14	US-10-205-823-412
6	800	60.6	1850	12	US-10-241-220-44
7	788	59.7	1066	13	US-10-098-841-71
8	749	56.7	969	11	US-09-796-753-55
9	713	54.0	806	12	US-10-241-220-45
10	560	42.4	1583	14	US-10-000-256A-32
11	302	22.9	693	10	US-09-934-249-14
12	178	13.5	467	11	US-09-918-995-2074
13	102	7.7	368	10	US-09-783-590-3464
14	50	3.8	65	10	US-09-783-590-3488
15	44	3.3	878	10	US-09-934-249-12
16	44	3.3	1713	11	US-09-796-753-57

17	41	3.1	475	10	US-09-934-249-15	Sequence 15, Appl
18	32	2.4	577	9	US-09-864-761-20542	Sequence 20542, A
19	32	2.4	1206	12	US-10-259-165-327	Sequence 327, App
20	32	2.4	1964	9	US-09-864-761-3776	Sequence 3776, Ap
21	29	2.2	401	9	US-09-864-761-3936	Sequence 3936, Ap
22	29	2.2	446	9	US-09-864-761-20699	Sequence 20699, A
23	29	2.2	1128	11	US-09-836-960-1	Sequence 1, Appl1
24	29	2.2	1277	13	US-10-062-254-279	Sequence 279, Appl
25	29	2.2	1570	11	US-09-836-960-4	Sequence 4, Appl1
26	29	2.2	2853	14	US-09-905-983-45	Sequence 45, Appl1
27	29	2.2	2853	14	US-10-117-293-42	Sequence 42, Appl
28	29	2.2	2887	12	US-10-017-621-89	Sequence 89, Appl
29	28	2.1	204	14	US-10-215-432-29	Sequence 29, Appl
30	28	2.1	251	14	US-10-060-036-418	Sequence 418, App
31	28	2.1	412	10	US-09-960-352-13161	Sequence 13161, A
32	28	2.1	496	10	US-09-783-590-3813	Sequence 3813, Ap
33	28	2.1	614	14	US-10-215-432-30	Sequence 30, Appl
34	28	2.1	614	14	US-10-215-432-31	Sequence 31, Appl
35	28	2.1	840	14	US-10-259-165-762	Sequence 762, App
36	28	2.1	1080	12	US-10-215-432-26	Sequence 26, Appl
37	28	2.1	15698	12	US-09-879-312-1	Sequence 1, Appl1
38	28	2.1	1303	10	US-10-311-455-2114	Sequence 2114, Ap
39	27	2.0	402	10	US-09-738-973-418	Sequence 418, App
40	27	2.0	402	10	US-09-854-133-418	Sequence 418, App
41	27	2.0	402	14	US-10-144-649A-418	Sequence 418, App
42	27	2.0	428	10	US-09-920-455-62	Sequence 62, Appl
43	27	2.0	1041	14	US-10-177-293-285	Sequence 285, App
44	27	2.0	1161	10	US-09-833-381-2046	Sequence 2046, Ap
45	27	2.0	1403	13	US-10-098-841-280	Sequence 280, App

ALIGNMENTS

US-09-934-249-1
Sequence 1, Application US/09934249
Patent No. US20020115081A1
GENERAL INFORMATION:
APPLICANT: Lee, Richard T.
APPLICANT: Landschulz, Katherine T.
APPLICANT: Turri, Thomas G.
APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
FILE REFERENCE: P0738/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934, 249
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227, 159
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1321
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (413)...(1273)
US-09-934-249-1

Query Match 100.0% Score 1321; DB 10; Length 1321;
Best Local Similarity 100.0% Pred. No. 0;
Matches 1321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CGACGCGGCTCGAGCGAAACCCGATCTCTTGACTTGATGAGAGAGAGCGG 60
DB	1	CGACGCGGCTCGAGCGAAACCCGATCTCTTGACTTGATGAGAGAGAGCGG 60
QY	61	CGGCGGCGGCGGCGGCGGAGCGGCTGCGTGGGGAAGCTACGCGAGAGCTACAGCCC 120
DB	61	CGGCGGCGGCGGCGGCGGAGCGGCTGCGTGGGGAAGCTACGCGAGAGCTACAGCCC 120

OY	12	GGGGGAGGCGGGGGCCCCGGCTGGCAGGCGCCATTTTCCGGAGCGCCACCGCGGGGACATGGCG	180
Db	121	GGCGGAGCGCGGGCCCCCGCTGGCAGGCGCCATTTTCCGGAGCGCCACCGCGGGGACATGGCG	180
OY	181	ACGGCCCCGGGGGCTGCCGAGGGGAGGCCGGGGGGGGCGCAGCGGAGCGCGGTCTCCGGCAC	240
Db	181	ACGGCCCCGGGGGCTGCCGAGGGGAGGCCGGGGGGGGCGCAGCGGAGCGCGGTCTCCGGCAC	240
OY	241	TGAGCCCCGGGGGGCCCCGGGGAACTTGGCGGGGACCGGAGCCGGGGAGCGCGGGGGGGCGG	300
Db	241	TGAGCCCCGGGGGGCCCCGGGGAACTTGGCGGGGACCGGAGCCGGGGAGCGCGGGGGGGCGG	300
OY	301	CTCCCGCGCGGGCGGCTCTCGCATGGGGGGGCCCAAGCTCCGGGGCGCGCGCGCGGAGCCCC	360
Db	301	CTCCCGCGCGGGCGGCTCTCGCATGGGGGGGCCCAAGCTCCGGGGCGCGCGCGCGGAGCCCC	360
OY	361	CCCCGGCGCCCCCGGAGCCCCCG	420
Db	361	CCCCGGCGCCCCCGGAGCCCCCG	420
OY	421	CTTGATGGGGGGTCAACAGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	480
Db	421	CTTGATGGGGGGTCAACAGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	480
OY	481	GTGCAACTGCMAAGCTCTTGTTCAGAGCATGAGATCAGGAGCTGAGTTGTTC	540
Db	481	GTGCAACTGCMAAGCGCTTGTTCAGAGCATGAGATCAGGAGCTGAGTTGTTC	540
OY	541	GATCATCATCATCGTGGTGGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	600
Db	541	GATCATCATCATCGTGGTGGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	600
OY	601	CCACTACAGCTGTCTGCACGCGCTTCATCAGCCGCGCAGCCAGCGGGGGCGGAGAGAGA	660
Db	601	CCACTACAGCTGTCTGCACGCGCTTCATCAGCCGCGCAGCCAGCGGGGGCGGAGAGAGA	660
OY	661	AGATGCCCTGTCTCAGAAAGATACCTGTGGCCCTCGGAGAGCACAAGTGTACGAGCAACGG	720
Db	661	AGATGCCCTGTCTCAGAAAGATACCTGTGGCCCTCGGAGAGCACAAGTGTACGAGCAACGG	720
OY	721	AATCCAGAGCGGAGGATGTCTAGGCGCGCGCTCGGCGCCACGACCGCGCTGGCGTGGCGCC	780
Db	721	AATCCAGAGCGGAGGATGTCTAGGCGCGCGCTCGGCGCCACGACCGCGCTGGCGTGGCGCC	780
OY	781	CTTGGCCCGAGGGGAGCGCTTCCACCGCTTCCAGCCCACTTATCCGTAACCTGTGACAGCAGA	840
Db	781	CTTGGCCCGAGGGGAGCGCTTCCACCGCTTCCAGCCCACTTATCCGTAACCTGTGACAGCAGA	840
OY	841	GATGACCTGTGCACACCATCTCGCTTCCAGAGGGGAGAGGCCCCACCTTACAGAGG	900
Db	841	GATGACCTGTGCACACCATCTCGCTTCCAGAGGGGAGAGGCCCCACCTTACAGAGG	900
OY	901	CCCCGTGACCTCCAGCTTTCGGGAGCCCGGAGCAGCAGCTGGAACCTGAAACCGGGAGTGGT	960
Db	901	CCCCGTGACCTCCAGCTTTCGGGAGCCCGGAGCAGCAGCTGGAACCTGAAACCGGGAGTGGT	960
OY	961	GCGGCGACCCCCCAACAGAACCACTTGTGACAGTGAACCTGATGGATATGTGCAAGCTGGG	1020
Db	961	GCGGCGACCCCCCAACAGAACCACTTGTGACAGTGAACCTGATGGATATGTGCAAGCTGGG	1020
OY	1021	CGGCGCTTCGCCCCCGCAGAGTAATCGGGGATCAGCGCCACAGTGTACGGCAGAGGGGG	1080
Db	1021	CGGCGCTTCGCCCCCGCAGAGTAATCGGGGATCAGCGCCACAGTGTACGGCAGAGGGGG	1080
OY	1081	GCGCATGAGAGGGGGCGCGCCCACTTACAGGAGGTCAATGGGCCACTACCGGGGGTCTCT	1140
Db	1081	GCGCATGAGAGGGGGCGCGCCCACTTACAGGAGGTCAATGGGCCACTACCGGGGGTCTCT	1140
OY	1141	CTTCCAGACACAGCAGAGCAGTGGGGCGCGCTCTTGTGGAGGGGAGCCCGGCTTCACACA	1200
Db	1141	CTTCCAGACACAGCAGAGCAGTGGGGCGCGCTCTTGTGGAGGGGAGCCCGGCTTCACACA	1200

QY	1201	CACACATATGCGCCCTTAGAGACGGACCATTTGGAGCAAAAGAAGTATAACAGAA	1260
Dδ	1201	CACACATATGCGGCCCTTAGAGACGGACCATTTGGAGCAAAAGAAGTATAACAGAA	1260
QY	1261	AGGACACCCTCTCTAGGGTCCCCAGGGGGGCGGGCTGGGGCTGCATTAGTGAAAAGGCA	1320
Dδ	1261	AGGACACCCTCTCTAGGGTCCCCAGGGGGGCGGGGCTGGGGCTGCATTAGTGAAAAGGCA	1320
QY	1321	G	1321
Dδ	1321	G	1321

RESULT 2
FE-10-34

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? Sequence 119, Application US/10241220
? Publication No. US20030148408A1
? GENERAL INFORMATION:
? APPLICANT: Frantz, Gretchen
? APPLICANT: Hillan, Kenneth J.
? APPLICANT: Phillips, Heidi
? APPLICANT: Polakis, Paul
? APPLICANT: Spencer, Susan
? APPLICANT: Williams, P. Mickey
? APPLICANT: Wu, Thomas
? APPLICANT: Zhang, Zemin
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
? TITRE OF INVENTION: TREATMENT OF TUMOR
? FILE REFERENCE: P5010R1-US
? CURRENT APPLICATION NUMBER: US/10/241,220
? CURRENT FILING DATE: 2002-12-13
? NUMBER OF SEQ ID NOS: 120
? SEQ ID NO 119
? LENGTH: 4839
? TYPE: DNA
? ORGANISM: Homo Sapien
US-10-241-220-119

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Query Match	93.0%	Score 1229;	DB 12;	Length 4839;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1229; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	93	GGAAAGCTAGGGGCGAGAGCTCAGCCCCGGGGGAGACGGGGCCCCGGCTGCAGGCACTT	152
Db	1	GGAAAGCTAGGGGCGAGAGCTCAGCCCCGGGGGAGACGGGGCCCCGGCTGCAGGCACTT	60
QY	153	TTCCGGAGCGCACCCGCGGGGCACTGCGACAGCCCCCGGGGCTGCCGAGGGGAGGCCGGG	212
Db	61	TTCCGGAGCGCACCCGCGGGGCACTGCGACAGCCCCCGGGGCTGCCGAGGGGAGGCCGGG	120
QY	213	GGGGCGACGGAGCGCGGTCCCGCGCACGTGAGCCCCGGGGGCGCCCCGGGAAATTGGCGGC	272
Db	121	GGGGCGACGGAGCGCGGTCCCGCGCACGTGAGCCCCGGGGGCGCCCCGGGAACTTGGCGGC	180
QY	273	GACCCGAGCCCCGAGCGCGGGGGCGCGCTCCCGCCGCGCGCGCTCTGCACTGCGGGGCG	332
Db	181	GACCCGAGCCCCGAGCGCGGGGGCGCGCTCCCGCCGCGCGCGCTCTGCACTGCGGGGCG	240
QY	333	CCCAAGCTCCGGGGCGCGCGCGCGAGCCCCCGGGGCGCCCCGAGCCCCCGCGCGCGCG	392
Db	241	CCCAAGCTCCGGGGCGCGCGCGCGAGCCCCCGGGGCGCCCCGAGCCCCCGCGCGCGCG	300
QY	393	GCGGGCGCGCGCGCGCTTCATATGACACGCTTATGGGGGTCAACAGCACCGCGCGCGCG	452
Db	301	GCGGGCGCGCGCGCGCTTCATATGACACGCTTATGGGGGTCAACAGCACCGCGCGCGCG	360
QY	453	CCGCCGGGAGCCCAATGCTCTCTGACAGTGCACACTGCACAAAGCTCTTTGTTCAGAGCA	512
Db	361	CCGCCGGGAGCCCAATGCTCTCTGACAGTGCACAAAGCTCTTTGTTCAGAGCA	420
QY	513	TGGAAATACAGAGAGCTGGAGTTTGTTCAGATATATATCTGGGGGGATGATAGGTGA	572
Db	421	TGGAAATACAGAGAGCTGGAGTTTGTTCAGATATATATCTGGGGGGATGATAGGTGA	480

OY		573	GGGAGGGGTATACAGGCCTGGTGAAGCCACTCAAAAGTGTCTGCACGGGTCCTCATACA	632
Dd		481	TGGTGTTGGTATACGTGCTCGTAGGCCACTCAAAAGTGTCTGCACGGTCTTCATACA	540
OY		633	GCCGGCACAGCAGGAGGGGCGAGAGAGAAGATGCCCCGTCTCTCAGAAAGGATGCTGTGGC	692
Dd		541	GCCGGCACAGCAGGAGGGGCGAGAGAGAAGATGCCCCGTCTCTCAGAAAGGATGCTGTGGC	600
OY		693	CCTCGGAGAGACACAGTGTCAAGGCAAGGAATCCACAGCCGACAGTCTACGCCCCCCTC	752
Dd		601	CCTCGGAGAGACACAGTGTCAAGGCAAGGAATCCACAGCCGACAGTCTACGCCCCCCTC	660
OY		753	GGCCACCAGAACGGCTGGCCGTGGCCGCTTGGCCAGCCGAGGAGCGGCTTCCACCGCTTCC	812
Dd		661	GGCCACCAGAACGGCTGGCCGTGGCCGCTTGGCCAGCCGAGGAGCGGCTTCCACCGCTTCC	720
OY		813	AGCCACACTTATCCGTACTGTGACGACAGAGATGCAGCTGCCACCACCATCTCGCTGTACAG	872
Dd		721	AGCCACACTTATCCGTACTGTGACGACAGAGATGCAGCTGCCACCACCATCTCGCTGTACAG	780
OY		873	ACGGGGAGAGAGCCCCCACCCTTACCAAGGGCCCCCTGCACCCTTCAGCTTGGGAGCCCGAGC	932
Dd		781	ACGGGGAGAGAGCCCCCACCCTTACCAAGGGCCCCCTGCACCCTTCAGCTTGGGAGCCCGAGC	840
OY		933	AGCAGCTGGAACTGAACCCGGGAGTGGGAGCGGACGCCAACCOCACAAAAGAAACCATCTTCAGCA	992
Dd		841	AGCAGCTGGAACTGAACCCGGGAGTGGGAGCGGACGCCAACCOCACAAAAGAAACCATCTTCAGCA	900
OY		993	GTCAGCTGATGTGATAGTGCACAGGCTGGGGGGCCCCCTGCCCCCAGCAGTAATACTGGGGCA	1052
Dd		901	GTCAGCTGATGTGATAGTGCACAGGCTGGGGGGCCCCCTGCCCCCAGCAGTAATACTGGGGCA	960
OY		1053	TCACAGCCACGTGCTAGGGCAGCGCGGGGGGCGCATATGAGAGGGGCGCGCCCACTACAGCG	1112
Dd		961	TCACAGCCACGTGCTAGGGCAGCGCGGGGGGCGCATATGAGAGGGGCGCGCCCACTACAGCG	1020
OY		1113	AGGTCATCGCGGCATACCCGGGGGTCTCTCTTCACAGACACAGCAGACAGTGGGCGGCCCT	1172
Dd		1021	AGGTCATCGCGGCATACCCGGGGGTCTCTCTTCACAGACACAGCAGACAGTGGGCGGCCCT	1080
OY		1173	CCTTGCTGAGAGGGAGCCCGGCTCCACACACACACATGCGGCCCTTAGAGAGCGACGCA	1232
Dd		1081	CCTTGCTGAGAGGGAGCCCGGCTCCACACACACACATGCGGCCCTTAGAGAGCGACGCA	1140
OY		1233	TCGTGAGCAAAAGAAAGGATTAACAGAAAGACACCCCTTAGGATCCCCAGGGGGGCC	1292
Dd		1141	TCGTGAGCAAAAGAAAGGATTAACAGAAAGACACCCCTTAGGATCCCCAGGGGGGCC	1200
OY		1293	GGGCTGGGGCTGCTAGGTGAAAAAGGCG	1321
Dd		1201	GGGCTGGGGCTGCTAGGTGAAAAAGGCG	1229
RESULT 3				
US-09-934-249-3				
Sequence 3, Application US/09934249				
Patent No. US20020115081A1				
GENERAL INFORMATION:				
APPLICANT: Lee, Richard T.				
APPLICANT: Landschultz, Katherine T.				
APPLICANT: Turf, Thomas G.				
APPLICANT: Thompson, John F.				
APPLICANT: Kennedy, Scott P.				
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF				
TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS				
FILE REFERENCE: P0738/7001/ERP/VA				
CURRENT FILING DATE: 2001-08-21				
PRIOR APPLICATION NUMBER: US 60/227,159				
PRIOR FILING DATE: 2000-08-22				
NUMBER OF SEQ ID NOS: 17				
SOFTWARE: FastSeq for Windows Version 3.0				

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: SEQ ID NO 3
: LENGTH: 861
: TYPE: DNA..
: ORGANISM: Homo Sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(861)
: OS=934-249-3

Query Match      65.2%; Score 861; DB 10; Length 861;
Best Local Similarity 100.0%; Pident. No. 0;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      413  ATGCACCGCTTGATGGGGGTCTAAAGACACCGCCCGCCCGCCGGGCGACGCCAATATC 472
Db       1  ATGCACCGCTTGATGGGGGTCTAAAGACACCGCCCGCCCGCCGGGCGACGCCAATATC 60

QY      473  TCCGACAGTGTCACTCAAAAGCTCTTTGTTCCAGAGCATGAGATCAGAGACTGGAG 532
Db      61  TCCGACAGTGTCACTCAAAAGCTCTTTGTTCCAGAGCATGAGATCAGAGACTGGAG 120

QY      533  TTTTTCAGATCATCATCATCTGCTGGTGTGATGATGTTGATGTTGTTGTTGATCAGTGC 592
Db     121  TTTGTTGATCATCATCATCATCTGCTGGTGTGATGATGTTGATGTTGTTGATCAGTGC 180

QY      593  CTGCTGAGCCACTCAAAAGCTGTCTGACAGGTTCCTTTCATCAGCCGGCACAGCCAGGGCGG 652
Db     181  CTGCTGAGCCACTCAAAAGCTGTCTGACAGGTTCCTTTCATCAGCCGGCACAGCCAGGGCGG 240

QY      653  AGGAGAGAAATGTCCTGTCTCTCAGAAAGATGCTGTGGCCCTGTGGAGAGCACAGTGTCA 712
Db     241  AGGAGAGAAATGTCCTGTCTCTCAGAAAGATGCTGTGGCCCTGTGGAGAGCACAGTGTCA 300

QY      713  GGCACAGGAATCCAGAGCCGACAGTCTACGCCCCGCTCGGCCACACGACCGCCTGACC 772
Db     301  GGCACAGGAATCCAGAGCCGACAGTCTACGCCCCGCTCGGCCACACGACCGCCTGACC 360

QY      773  GTGGCCGCTTTCGGCCAGCGGGGAGCGCTTCACCGGCTTCCAGCCGCTACCTATCCGTACTG 832
Db     361  GTGGCCGCTTTCGGCCAGCGGGGAGCGCTTTCACCGGCTTCCAGCCGCTACCTATCCGTACTG 420

QY      833  CAGCAGCAGATGACACTGTCCACCCACCATCTCGCTGTCTGACAGCGGGGAGAGACCCCCACC 892
Db     421  CAGCAGCAGATGACACTGTCCACCCACCATCTCGCTGTCTGACAGCGGGGAGAGACCCCCACC 480

QY      893  TACCAAGGCGCCTGCACCTTCACGCTTCGAGTGGAGCCCGACGACAGCTGGAATGAACCGG 952
Db     481  TACCAAGGCGCCTGCACCTTCACGCTTCGAGTGGAGCCCGACGACAGCTGGAATGAACCGG 540

QY      953  GAGTCGGGTGGCGGACCCCGCAAAAGAACATCTTCCAGCATGTGACCTGATGGATATGAGCC 1012
Db     541  GAGTCGGGTGGCGGACCCCGCAAAAGAACATCTTCCAGCATGTGACCTGATGGATATGAGCC 600

QY      1013  AGGCTGGGGCGGCCCTTGCCGCCCGCCAGCATGTAATCGGGGACATCAGCGCCATGCTACGGC 1072
Db     601  AGGCTGGGGCGGCCCTTGCCGCCCGCCAGCATGTAATCGGGGACATCAGCGCCATGCTACGGC 660

QY      1073  AGCGGCGGGCGCATGAGAGGGGCGCGCCACCTACAGCAGAGGTTCATCGGCCACTTACCGG 1132
Db     661  AGCGGCGGGCGCATGAGAGGGGCGCGCCACCTACAGCAGAGGTTCATCGGCCACTTACCGG 720

QY      1133  GGGGTCTCTCTTCCAGACACACAGACAGAGTGGGGCGCCCTCTCTGTCTGTGAGAGGACCCGG 1192
Db     721  GGGGTCTCTCTTCCAGACACACAGACAGAGTGGGGCGCCCTCTCTGTGTGAGAGGACCCGG 780

QY      1193  CTCACACACACACATGCGCCCGCTAGAGAGCCAGGCATCTGGAGCAAGAGAGAGAT 1252
Db     781  CTCACACACACACATGCGCCCGCTAGAGAGCCAGGCATCTGGAGCAAGAGAGAGAT 840

QY      1253  AAACAGAAAGGACACCTCTTC 1273
Db     841  AAACAGAAAGGACACCTCTTC 861

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RESULT 4
US-10-301-822-208
; Sequence 208, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangl
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgess, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (96)...(854)
US-10-301-822-208

Query Match 60.6%; Score 800; DB 12; Length 1141;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 CGGAGCTGAGATTGTTTCAGATCATCATCTCGTGGTGGTGGTGGTGGTGGTGG 581
DB 100 CGGAGCTGAGATTGTTTCAGATCATCATCTCGTGGTGGTGGTGGTGGTGGTGG 159
QY 582 TGATCAGTGTGCTGTGAGGACATCAAGAGTGTGAGGAGTGTGAGGAGTGTGAGGAG 641
DB 160 TGATCAGTGTGCTGTGAGGACATCAAGAGTGTGAGGAGTGTGAGGAGTGTGAGGAG 219
QY 642 GCCAGGGGCGAGAGAGAGATGCTGTCTCAGAAAGATGCTGTGAGGAGTGTGAGGAG 701
DB 220 GCCAGGGGCGAGAGAGAGATGCTGTCTCAGAAAGATGCTGTGAGGAGTGTGAGGAG 279
QY 702 GCACAGTGTGACGAGCAAGCAATCCAGAGCGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAG 761
DB 280 GCACAGTGTGACGAGCAAGCAATCCAGAGCGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAG 339
QY 762 ACCGCTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAG 821
DB 340 ACCGCTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAG 399
QY 822 ATCCGTACGTGACAGCAGATGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAG 881
DB 400 ATCCGTACGTGACAGCAGATGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAG 459
QY 882 AGCCCCACCTTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 941
DB 460 AGCCCCACCTTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 519
QY 942 AACTGAACCGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1001
DB 520 AACTGAACCGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 579

QY 1002 TGATATGTCAGAGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1061
DB 580 TGATATGTCAGAGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 639
QY 1062 CGTGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1121
DB 640 CGTGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 699
QY 1122 GCCACTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1181
DB 700 GCCACTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 759
QY 1182 AGGGAGCCGGGCTCCACACACACATGCGGCGCTTAGAGAGCGAGCATCTGAGAGA 1241
DB 760 AGGGAGCCGGGCTCCACACACACATGCGGCGCTTAGAGAGCGAGCATCTGAGAGA 819
QY 1242 AAGAGAAGATTAACGAAAGAGACCTCTCTAGGAGTCCCAAGAGGAGGAGGAGGAGGAGGAG 1301
DB 820 AAGAGAAGATTAACGAAAGAGACCTCTCTAGGAGTCCCAAGAGGAGGAGGAGGAGGAGGAG 879
QY 1302 CTGCTAGGATGAAGAGGAG 1321
DB 880 CTGCTAGGATGAAGAGGAG 899

RESULT 5
US-10-205-823-412
; Sequence 412, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangl
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glatz, Karen
; APPLICANT: Zhao, Xunel
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-04
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 412
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-412

Query Match 60.6%; Score 800; DB 14; Length 1141;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 CGGAGCTGAGATTGTTTCAGATCATCATCTCGTGGTGGTGGTGGTGGTGGTGG 581
DB 100 CGGAGCTGAGATTGTTTCAGATCATCATCTCGTGGTGGTGGTGGTGGTGGTGG 159


```

? APPLICANT: Asundi, Vinod
? APPLICANT: Xu, Chongjun
? APPLICANT: Zhou, Ping
? APPLICANT: Ma, Yunding
? APPLICANT: Wang, Jian-Rui
? APPLICANT: Zhao, Qing A.
? APPLICANT: Ren, Feiyang
? APPLICANT: Chen, Rui-hong
? APPLICANT: Wang, Duncui
? APPLICANT: Wang, Zhiwei
? APPLICANT: Wehrman, Tom
? APPLICANT: Zhang, Jie
? APPLICANT: Qian, Xiaohong B.
? APPLICANT: Drmanac, Radoje T.
? TITLE OF INVENTION: No. US20020197679a1 Nucleic Acids and
? FILE REFERENCE: 784CIP2
? CURRENT APPLICATION NUMBER: US/10/098,841
? CURRENT FILING DATE: 2002-03-13
? PRIOR APPLICATION NUMBER: 09/598,042
? PRIOR FILING DATE: 2000-06-20
? PRIOR APPLICATION NUMBER: 09/552,317
? PRIOR FILING DATE: 2000-04-25
? PRIOR APPLICATION NUMBER: 09/488,725
? PRIOR FILING DATE: 2000-01-21
? NUMBER OF SEQ ID NOS: 331
? SOFTWARE: pc_files Version 1.0
? Seq ID NO 71
? LENGTH: 1066
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (134)..(867)
US-10-098-841-71

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[illegible]

Dd		605	GCGTGGGCGGCCCTGCCCCCCCAGCACTAATCTGGGCATAGGCCACGTGCTAACGGCA	664
OY		1074	GC GGCGGGCCGTCATGAGAGGGGCGCGCCACCTACAGCAGGATCGGCCACTACC	664
Dd		665	GC GCGGGGCGCATGAGAGGGGCGCGCCACCTACAGGAGATCATCGGCCACTACC	724
OY		1134	GGTCTCTCTTCACACACAGAGAGAGAGTAGTGCGCCCTCTTCTGTGAGAGGGGACCCGGC	1193
Dd		725	GGTCTCTCTTCACACACAGAGAGAGAGTAGTGCGCCCTCTTCTGTGAGAGGGGACCCGGC	784
OY		1194	TCCACACACACATCGCGCGCCCTTAGAGAGCGCAGCATCTGGAGCAAAGAGAAGATA	1253
Dd		785	TCCACACACACATCGCGCGCCCTTAGAGAGCGCAGCATCTGGAGCAAAGAGAAGATA	844
OY		1254	AACGAAGAGACACCTCTCTTAAGGGTCCCGCAGGGGGGCGGCGTGGGGCTGCGTAGTGA	1313
Dd		845	AACGAAGAGACACCTCTCTTAAGGGTCCCGCAGGGGGGCGGCGTGGGGCTGCGTAGTGA	904
OY		1314	AAAGCAG 1321	
Dd		905	AAAGCAG 912	
 RESULT 8 US-09-796-753--55 ; Sequence 55, Application US/09796753 ; Publication No. US20030027988A1 ; GENERAL INFORMATION: ; APPLICANT: McCarthy, Sean A. ; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF ; FILE REFERENCE: 7853-227-999 ; CURRENT APPLICATION NUMBER: US/09/796,753 ; PRIOR FILING DATE: 2001-03-01 ; PRIOR APPLICATION NUMBER: 09/183,175 ; PRIOR FILING DATE: 1998-10-30 ; PRIOR APPLICATION NUMBER: 09/223,094 ; PRIOR FILING DATE: 1998-12-30 ; PRIOR APPLICATION NUMBER: 09/223,546 ; PRIOR FILING DATE: 1998-12-30 ; PRIOR APPLICATION NUMBER: 09/224,246 ; PRIOR FILING DATE: 1998-12-30 ; PRIOR APPLICATION NUMBER: 09/259,388 ; PRIOR FILING DATE: 1999-02-26 ; PRIOR APPLICATION NUMBER: 60/122,458 ; PRIOR FILING DATE: 1999-03-01 ; PRIOR APPLICATION NUMBER: 09/312,359 ; PRIOR FILING DATE: 1999-05-14 ; PRIOR APPLICATION NUMBER: 09/336,536 ; PRIOR FILING DATE: 1999-06-18 ; PRIOR APPLICATION NUMBER: 09/342,687 ; PRIOR FILING DATE: 1999-06-29 ; PRIOR APPLICATION NUMBER: 09/345,464 ; PRIOR FILING DATE: 1999-06-30 ; PRIOR APPLICATION NUMBER: 09/365,164 ; PRIOR FILING DATE: 1999-07-30 ; PRIOR APPLICATION NUMBER: 09/399,723 ; PRIOR FILING DATE: 1999-09-20 ; PRIOR APPLICATION NUMBER: 09/409,634 ; PRIOR FILING DATE: 1999-09-30 ; PRIOR APPLICATION NUMBER: 09/471,179 ; PRIOR FILING DATE: 1999-12-23 ; PRIOR APPLICATION NUMBER: 09/474,071 ; PRIOR FILING DATE: 1999-12-29 ; PRIOR APPLICATION NUMBER: 09/474,072 ; PRIOR FILING DATE: 1999-12-29 ; PRIOR APPLICATION NUMBER: 09/514,010 ; PRIOR FILING DATE: 2000-02-25 ; PRIOR APPLICATION NUMBER: 09/516,745 ; PRIOR FILING DATE: 2000-03-01 ; PRIOR APPLICATION NUMBER: 09/522,002 ; PRIOR FILING DATE: 2000-05-14 ; PRIOR APPLICATION NUMBER: 09/597,993				

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10-000-256A-32
 Publication No. US2003003983A1
 GENERAL INFORMATION:
 APPLICANT: Sun, Yongming
 APPLICANT: Recipon, Hervé
 APPLICANT: Chen, Sel-Yu
 APPLICANT: Iiu, Chenghua
 TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
 FILE REFERENCE: DEX-0259
 CURRENT APPLICATION NUMBER: US/10/000,256A
 CURRENT FILING DATE: 2001-11-01
 PRIOR APPLICATION NUMBER: 60/244,782
 PRIOR FILING DATE: 2000-11-01
 NUMBER OF SEQ ID NOS: 240
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 32
 LENGTH: 1583
 TYPE: DNA
 ORGANISM: Homo sapien
 US-10-000-256A-32

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Db	1067	CCCAAACAGAACCATCTTTCGACAGTAGTACCTGATGTGATTGATGGCCAGGCTGGGGGCCCTGT	1126			
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Dp	1247 CGACGAGACAGTGGGGCGCCCTCTTCTGTGAGGSGACCCGGCTCCACACACACAT	1308
QY	1210 CGCGCCCTTAGAGACGCGACCATGTGGAGCAAGAGAGATTAACAGAAAGACACC	1265
Dp	1307 CGGCCCCCTTAGAGAGGCGACCACTTGGAGCAAGAGAGATTAACAGAAAGACACC	1364
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US-09-934-249-14/c
; Sequence 14, Application US/09934249
; Patent No. US20020115081A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Richard T.
; APPLICANT: Landschulz, Katherine T.
; APPLICANT: Tuft, Thomas G.
; APPLICANT: Thompson, John P.
; APPLICANT: Kennedy, Scott P.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
; FILE REFERENCE: P0738/7001/EP/KA
; CURRENT APPLICATION NUMBER: US/09/934,249
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/227,159
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (639)...(639)
; OTHER INFORMATION: a, c, g, or t/u
US-09-934-249-14

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Thu Aug 28 08:39:18 2003

us-09-934-249-1.01i8.rnpb

Page 10

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RESULT 15
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Sequence 12, Application US/09934249
Patent NO. US20020115081A1
GENERAL INFORMATION:
APPLICANT: Lee, Richard T.
APPLICANT: Landschulz, Katherine T.
APPLICANT: Turl, Thomas G.
APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
TITLE OF INVENTION:
FILE REFERENCE: P0738/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 878
TYPE: DNA
ORGANISM: Mus Musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (20)...(841)
US-09-934-249-12

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Best Local Similarity 100.0%; Pred. No. 2,2e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: August 28, 2003, 01:25:41
Job time : 372 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2003, 17:38:05; Search time 5026 Seconds

(without alignments)
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Title: US-09-934-249-1

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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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6	800	60.6	1818	9	AY128643 Homo sapi
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ALIGNMENTS

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DEFINITION Sequence 1 from Patent WO0216416.
ACCESSION AX392417
VERSION AX392417.1 GI:19700732
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 Lee R.T., Landschulz K.T., Kennedy S.P., Thompson J.F. and
Turi T.G.
TITLE Diagnosis and treatment of cardiovascular conditions

JOURNAL Patent: NO 0216416-A 1 28-FEB-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. (US)
FEATURES Location/Qualifiers

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BASE COUNT 223 a 493 c 440 g 165 t

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Very Match 100.0%; Score 1321; DB 6; Length 1321;
Best Local Similarity 100.0%; Pred. No. 1.9e-176;
Matches 1321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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DEFINITION AF305616.1 GI:16303741
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS
TITLE
CHARACTERIZATION OF A NOVEL GENE, STAG1/PMEP1, UPREGULATED IN
RENAL CELL CARCINOMA AND OTHER SOLID TUMORS
MOL. CARCINO. 32 (1), 44-53 (2001)
JOURNAL
MEDLINE
PUBMED
11568975
2 (pages 1 to 4839)
Rae, F.K., Hooper, J.D., Nicol, D.L. and Clements, J.A.
DIRECT SUBMISSION
Submitted (14-SEP-2000) Centre for Molecular Biotechnology,
Queensland University of Technology, 2 George St, Brisbane, QLD
4001, Australia
Location/Qualifiers
1. .4839
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/mol_type="mRNA"

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 4818..4823
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Best Local Similarity 100.0%; Pred. No. 1,3e-163; Mismatches 0; Indels 0; Gaps 0;

Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 61 TTCCGGAGCGGAGCGGCGGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 120

213 GGGCGGAGCGGAGCGGCGGCGGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 272
 121 GGGCGGAGCGGAGCGGCGGCGGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 180

273 GACCGGAGCGGAGCGGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 332
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333 CCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 392
 241 CCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300

393 GCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 452
 301 GCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360

453 CCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 512
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 841 AGCAGCTGAG 900

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RESULT 3
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 ACCESSION
 VERSION
 KEYWORDS
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 ORGANISM
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 (bases 1 to 1061)
 Strausberg, R.
 Direct Submission
 Submitted (15-OCT-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-7590,
 USA
 NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 Contact: MGC help desk
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 CDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (TLNL)
 BC Cancer Agency, Vancouver, BC, Canada
 info@bcgsc.bc.ca

REMARK
 COMMENT
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
 Leticia Hsiao, Martin Kizylinski, Reta Kutsche, Oliver Lee, Soo
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
 Ness, Pawan Pandoh, Anna-Liisa Prabh, Parvaneh Saeedi, Jacqueline
 Schein, Diane Smalhus, Michael Smith, Lorraine Spence, Jeff Stott,
 Michael Thorne, Miranada Tsai, Natassja van den Bosch, Jill Vardy,
 George Yang, Scott Zuyderduyn, Marco Marra.

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Qy	1159	CAGTGGGCGCGCCCTCTTTCGTGAGGAGGGGACCCGGCTCCACACACACATCGCGCCCT	1218
Db	737	CAGTGGGCGCGCCCTCTTTCGTGAGGAGGGGACCCGGCTCCACACACACATCGCGCCCT	796
Qy	1219	AGAGAGCGCACTCTTGAGCAAAAGAAAGATAAACAAGAAAGGACACCTCTCTAGGG	1278
Db	797	AGAGAGCGCACTCTTGAGCAAAAGAAAGATAAACAAGAAAGGACACCTCTCTAGGG	856
Qy	1279	TCGCCAGGGGGCGGGGCTGGGAGCTGCGTAGGTAAAGGCGAG	1321
Db	857	TCGCCAGGGGGCGGGGCTGGGAGCTGCGTAGGTAAAGGCGAG	899

SUBMITTER: 6
 ID: 28643
 US
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 ACCESSION: AY128643
 VERSION: AY128643.1 GI:22121998
 1818 bp mRNA linear PRI 10-APR-2003

ORGANISM	SOURCE
Homo sapiens (human)	
Homo sapiens	
Chordata: Vertebrata: Euteleostomi; teleostei: Osteichthyes: Actinopterygii: Cyprinodontiformes: Poeciliidae: Gambusia affinis holbrooki	

REFERENCE
1 (bases 1 to 1818)
AUTHORS
Brunschwig, E. B., Wilson, K., Mack, D., Dawson, D., Lawrence, E.,
Datta, D. M., Switzer, S., Beard, L.

TITLE	ABSTRACT
PMEPAL, a transforming growth factor-beta-induced marker of epithelial mesenchymal transition whose expression is maintained	

JOURNAL Cancer Res. 63 (7), 1568-1575 (2003)

REFERENCE 2 (bases 1 to 1818)

Lutterbaugh, J.D., Willis, C., Placzek, F. and Munkres, C.

Reserve University/Howard Hughes Medical Institute, 11001 Cedar Ave., Cleveland, OH 44106, USA

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"Howo andleng"

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CDS 145.858

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Db

104 CGAGCGTGGAGTTTGTTCAGATCATCATCTGCTGGTGAATGATGGATGGTGG 163

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Db 224 GCCAGGGCGAGAGAGATGCCCTGTCTCAGAGGATGCCCTGGCGAGA 283

384 CCACTGTAGGTAACGGAATCCAGAGCCCGCAGGCTACGCCCGGCTCGGCCACCG 343

||||| 403

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QY

882 AGCCCCACCTACCAAGGGCCCTGCACCCCTCCAGCTTCGGGACCCGAGCAGCAGC 311

942 AACTGACC GGAGTGGTGCGCGCACCCCAACAGAACCATCTTGACAGTGACCTGA 100

1003 TGCATAGTCCAGGCTGGGGGCCCCCTGCCCCCCCAGCAGTAACTCGGGCATCAGGCCA 106

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РЕЗУЛТАТ 7

DEFINITION Mus musculus, similar to transmembrane, prostate androgen induced

KEYWORDS
VERSION BC030993.1 GI:2000110

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Muraeniformes; Muraenidae; Muraeninae; Muraenini; Muraenini;

AUTHORS	CLASSBEG/AN	DATE	TIME	REMARKS
TITLE	Direct Submission			

Accession	Sequence	Length
Db	57652 CGGCGCATGGAGGGGCGCCGCCACACTACAGCGAGTCAATGCGCCACTACCCGGGGTTC	57711
QY	1138 CTCCTTCACGACACGAGAGCAAGTGGGCGCCCTCTCTGTCAGAGAGGAGACCCGGGTCCA	1197
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QY	1258 GAAAGGACACCCCTCTAGGCTCCCAAGGGGGGCGGGGCGGGGCGCTAGGTGGAAGAAG	1317
Db	57832 GAAAGGACACCCCTCTAGGCTCCCAAGGGGGGCGGGGCGGGGCGCTAGGTGGAAGAAG	57891
QY	1318 GCAG 1321	
Db	57892 GCAG 57895	

DLT 10
1977/8

LOCUS	130435 bp	DNA	linear	PRI 24-FEB-2001
DEFINITION	Human DNA sequence from clone RP4-718U7 on chromosome 22			

SOURCE *Homo sapiens* (human)

REFERENCE
AUTHORS
TITLE
JOURNAL

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 130435)
Sehra, H.
Direct Submission
Submitted (23-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,

COMMENT

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone con15s of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/BCP/Chr20> This sequence is the entire insert of clone RP4-718U7 The true left end of clone RP5-100T7B5 is at 71437 in this sequence. The true right end of clone RP4-579F20 is at 43945 in this sequence. RP4-718U7 is from the library RPCR1-4 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/dacpac/home.htm> VECTOR: pCYPAC2

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least

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one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest.
location/qualifiers
1. .130435
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repeat_region	2028. .2632	
repeat_region	2087. .2257	
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repeat_region	2583. .2716	
repeat_region	3378. .3426	
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repeat_region	5331. .5793	
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Query Match 45.0%; Score 594.4; DB 9; Length 130435;
Best Local Similarity 99.0%; Pred. No. 1.1e-74;
Matches 598; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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RESULT 11
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LOCUS Sequence 32 from Patent WO242776.
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ACCESSION AX593655
VERSION AX593655.1 GI:28375034
KEYWORDS
SOURCE
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1
Sup. Y., Recipon, H., Chen, S.Y. and Liu, C.
Compositions and methods relating to prostate specific genes and
proteins Patent: WO 0242776-A 32 30-MAY-2002;
Diadexus, Inc. (US)
FEATURES
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repeat_region	/note="L2 repeat: matches 2358. .2411 of consensus"
repeat_region	20264. .20432
repeat_region	/note="L2 repeat: matches 2581. .2750 of consensus"
repeat_region	20530. .21282
repeat_region	/note="L1MD2 repeat: matches 5595. .6341 of consensus"
repeat_region	21980. .22192
repeat_region	/note="L2 repeat: matches 2322. .2562 of consensus"
repeat_region	23102. .23203
repeat_region	/note="MIR repeat: matches 117. .218 of consensus"
repeat_region	23231. .23438
repeat_region	/note="MER20 repeat: matches 3. .218 of consensus"
repeat_region	23439. .23512
repeat_region	/note="MIR repeat: matches 182. .257 of consensus"
repeat_region	24460. .24580
repeat_region	/note="L1MD1 repeat: matches 6102. .6221 of consensus"
repeat_region	24752. .25042
repeat_region	/note="L2 repeat: matches 2386. .2709 of consensus"
repeat_region	2508. .25295
repeat_region	/note="MIR repeat: matches 61. .155 of consensus"
repeat_region	26450. .26485
repeat_region	/note="18 copies 2 mer tg 97% conserved"
repeat_region	29374. .29501
repeat_region	/note="MIR repeat: matches 55. .190 of consensus"
repeat_region	29350. .29728
repeat_region	/note="MIR repeat: matches 69. .248 of consensus"
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Best Local Similarity	99.6%; Pred. No. 1.3e-64;
Matches 524:	Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY	61 CGGCGGGGGGGGGGGGAGGAGCGCTGCGTGGGGAAGCTAGCGGAGAGGCTCAGCCCC 120
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DB	GGCGGAGCGCGCCCGCTGCGACCCATTTCGGGAGCGGACCCGGGGGACATGGCG 52717
QY	181 ACGCCCCGGGGCTGCCGAGGAGGAGCGGGGGGCGGAGCGAGCGCGCTCCCGCGAC 240
DB	ACGCCCCGGGGCTGCCGAGGAGGAGCGGGGGGCGGAGCGAGCGCGCTCCCGCGAC 52657
QY	241 TGAAGCCCGGGGGCCCCGGGAATTGGCGGCGACCCGAGCCCGGGGAGACCGGGCGGGC 300
DB	TGAAGCCCGGGGGCCCCGGGAATTGGCGGCGACCCGAGCCCGGGGAGACCGGGCGGGC 52597
QY	301 CTCCCGCGCGCGGCTCTCTGCACTGGGGGGCCCAAGCTCCGAGGCCCGCGCGAGCCCC 360
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QY	361 CCGCGCGCGCCCCCGGAGCCCCCGCGCCGCGCGCGCGCGCGCGCGCTGCATGCAACCG 420
DB	CCGCGCGCGCCCCCGGAGCCCCCGCGCCGCGCGCGCGCGCGCGCGCTGCATGCAACCG 52477
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DB	CTGATGGGGGTCAAGAGCAACCGCGCGCGCGCGCGCGCGCGGACCGCAATGCTCCGCA 52417
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19070. .19291
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19954. .20005
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20264. .20432
/note="L2 repeat: matches 2581. .2750 of consensus"
20530. .21882
/note="L1M2 repeat: matches 5595. .6341 of consensus"
21980. .22192
/note="L2 repeat: matches 2322. .2562 of consensus"
23102. .23203
/note="MIR repeat: matches 117. .218 of consensus"
23231. .23438
/note="MER20 repeat: matches 3. .218 of consensus"
23439. .23512
/note="MIR repeat: matches 182. .257 of consensus"
24460. .24580
/note="L1M1 repeat: matches 6102. .6221 of consensus"
24752. .25042
/note="L2 repeat: matches 2386. .2709 of consensus"
25208. .25295
/note="MIR repeat: matches 61. .155 of consensus"
26450. .26485
/note="18 copies 2 mer tg 97% conserved"
29374. .29501
/note="MIR repeat: matches 55. .190 of consensus"
29550. .29728
/note="MIR repeat: matches 59. .248 of consensus"

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Query Match	39.6%;	Score 522.8;	DB 9;	Length 150224;
Best Local Similarity	99.6%;	Pred. No. 1.3e-64;		
Matches 524;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;

Best Local similarity	20.00	20.00	20.00
Matches	524	Conservative	0
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RESULT 13
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 ACCESSION AX392430
 VERSION AX392430.1 GI:19700746
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 Lee, R.T., Landschulz, K.T., Kennedy, S.P., Thompson, J.F. and Turi, T.G.
 TITLE Diagnosis and treatment of cardiovascular conditions
 JOURNAL Patent: WO 0216416-A 14 28-FEB-2002
 THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. (US)
 FEATURES
 source 1..693
 Location/Qualifiers
 BASE COUNT 101 a 205 c 237 g 149 t 1 others
 ORIGIN
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 Best Local Similarity 97.4%; Pred. No. 4.2e-60;
 Matches 533; Conservative 0; Mismatches 10; Indels 4; Gaps 3;

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 QY 956 TCGGTGCGCGACCCCAACAGACCATCTTCAGACTGACCTGATGATAGTGCAGG 1015
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 DB 456 CTGGCGCGCCCTTCGCGCCAGCGAGCTTCACCGCTTCACGCCACCTGAGCGAGC 397
 QY 1076 GCGCGCGCATGAGAGGCGCGCGCCACTACAGAGCTCATCGGCGCATACCGGCGG 1135
 DB 396 GCGCGCGCATGAGAGGCGCGCGCGCCACTACAGAGCTCATCGGCGCATACCGGCGG 337
 QY 1136 TCTCTCTTCAGCAGCAGCAGAGAGTGGCGCGCTTCCTTCTGGA-GGGAGCCGGCT 1194
 DB 336 TCTCTCTTCAGCAGCAGCAGAGAGTGGCGCGCTTCCTTCTGGAAGGGAGACGGGTT 277
 QY 1195 CCACACACACATCGGCGCCCTTACAGAGCGGAGCTTCGAGCAAGAGAGATTA 1254
 DB 276 CCGCCACACACATCGGCGCCCTTACAGAGCGGAGCTTCGAGCAAGAGAGATTA 217
 QY 1255 ACAGAAAGGACACCTCTCTAGGGTCCCGAGGGGGCGGGCTGGGGTGGGTAGTAA 1314
 DB 216 ACAGAAAGGACACCTCTCTAGGGTCCCGAGGGGGCGGGCTGGGGTGGGTAGTAA 157
 QY 1315 AAGGAG 1321
 DB 156 AAGGAG 150

AF220208
 LOCUS AF220208 651 bp mRNA linear ROD 05-MAR-2001
 DEFINITION Mus musculus Nedd4 WW domain-binding protein 4 mRNA, partial cds.
 ACCESSION AF220208
 VERSION AF220208.1 GI:12004973
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murine; Mus.
 REFERENCE 1 (bases 1 to 651)
 Jolliffe, C.N., Harvey, K.F., Haines, B.P., Parasiyam, G. and Kumar, S.
 TITLE Identification of multiple proteins expressed in murine embryos as binding partners for the WW domains of the ubiquitin-protein ligase Nedd4
 JOURNAL Blochem. J. 351 Pt 3, 557-565 (2000)
 MEDLINE 20498735
 PUBMED 11042109
 REFERENCE 2 (bases 1 to 651)
 Jolliffe, C.N. and Kumar, S.
 TITLE Direct Submission
 JOURNAL Submitted (30-DEC-1999) Division of Haematology, Hanson Centre for Cancer Research, IMVS, Frome Rd, Adelaide, SA 5000, Australia
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 BASE COUNT 146 a 234 c 176 g 95 t
 ORIGIN
 Query Match 32.2%; Score 425; DB 10; Length 651;
 Best Local Similarity 83.2%; Pred. No. 1.9e-50;
 Matches 530; Conservative 0; Mismatches 80; Indels 27; Gaps 3;

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 DB 1 AGCCAGGCGCGAGAGAGAGAGTGCCTGCTCAGAGAGTGCCTGTGCGCGAG 60
 QY 701 AGCAGAGTGTAGGACGACGATCCAGAGCGGAGTCTAGCCCGCGCGCGCGAC 760
 DB 61 AGTACGGTGTCAAG---TGAAATGCCGAGCCACAGGTCTATGCCCGCGCGCG 117
 QY 761 GACCGCTGCGCGTGCCTCCCTTCGCGCGAGCGGAGCGCTTCCACCGCTTCAGCGCAC 820
 DB 118 GACCGCTGCGCGTGCCTCCCTTCGCGCGAGCGGAGCGCTTCCACCGCTTCAGCGCAC 168
 QY 821 TATCGTACCTTCAGCAGCAGAGTGCCTGCCACCCACCATCTGCTGTCAAGCGGAG 880
 DB 169 TACCCCTACCTTCAGCAGCAGAGTGCCTGCCACCCACCATCTGCTGTGATGGAG 228
 QY 881 GAGCGCCGACCTTACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 940
 DB 229 GAGCGCCGACCTTACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 288
 QY 941 GAATGAAACCGGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1000
 DB 289 GAGTGAACCGGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 348
 QY 1001 ATGATAGTCCAGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1060

RESULT 14

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 27, 2003, 17:37:20 ; Search time 418 Seconds

(without alignments)
8530.999 Million cell updates/sec

Title: US-09-934-249-1

Perfect score: 1321
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

al number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1321	100.0	1321	24	ABK12137	Human CDNA encodin
2	803.2	60.8	969	21	AAA75151	CDNA encoding a hu
3	802.2	60.7	1140	21	ABK92120	Prostate cancer-as
4	801.6	60.7	969	21	AAA75163	CDNA clone encodin
5	801.6	60.7	969	21	AAA75164	CDNA clone encodin
6	801.6	60.7	969	21	AAA75165	CDNA clone encodin
7	800.6	60.6	1061	21	AAA47429	Sequence encoding
8	800.6	60.6	1334	25	ABZ36103	Human secretory po

9	790.4	59.8	1066	22	AA157868	Human polynucleoti
10	760	57.5	1069	22	AA159654	Human polynucleoti
11	616.4	46.7	878	24	ABK12142	Mouse CDNA encodin
12	589.2	44.6	1583	24	ABK61424	Prostate specific
13	493.6	37.4	693	24	ABK12143	Human MIVR-1 homol
14	466.2	35.3	1713	21	AAA75152	CDNA encoding a mu
15	464.6	35.2	1713	21	AAA75166	CDNA clone encodin
16	464.6	35.2	1713	21	AAA75167	CDNA clone encodin
17	464.6	35.2	1713	21	AAA75168	CDNA clone encodin
18	417.8	31.6	812	20	AA252964	Human prostate tum
19	417	31.6	474	25	ABZ84732	Toxicologically re
20	401.4	30.4	408	22	AA65983	Novel Human polynu
21	400.6	30.3	673	24	ABT09178	Phase-1 Rat CT gen
22	352.2	26.7	8494	23	AA577304	DNA encoding novel
23	351.6	26.6	937	21	AA252507	Human secreted pro
24	350.4	26.5	1879	23	AA584503	DNA encoding novel
25	350	26.5	920	24	ABK34251	Human CDNA for nov
26	349	26.4	8065	19	AAV38335	Manic-depressive I
27	349	26.4	8093	24	ABK12145	Human MIVR-1 homol
28	341.8	25.9	475	24	ABK12144	Human MIVR-1 homol
29	333.8	25.3	8103	23	AA577312	DNA encoding novel
30	298	22.6	837	24	ABQ43498	Oligonucleotide fo
31	284.2	22.6	837	24	ABQ43499	Oligonucleotide fo
32	284.2	21.5	8440	23	AA577305	DNA encoding novel
33	284.2	21.5	8440	24	ABK83477	Human CDNA differe
34	281	21.3	8011	19	AAV38336	Manic-depressive I
35	270.8	20.5	837	24	ABQ43500	Oligonucleotide fo
36	270.8	20.5	837	24	ABQ43501	Oligonucleotide fo
37	252.6	19.1	8041	23	AA577310	DNA encoding novel
38	232	17.6	254	21	AAA41265	Human secreted exp
39	223.4	16.9	1428	23	AA592497	DNA encoding novel
40	223.4	16.9	2942	23	AA577313	DNA encoding novel
41	100.2	7.6	522	24	ABT10027	Human breast cance
42	92	7.0	426	23	AA584502	DNA encoding novel
43	84.6	6.4	114955	20	AA533491	Human adenosine Al
44	79	6.0	114955	20	AA533491	Human adenosine Al
45	78.6	6.0	40668	24	ABQ88150	Human osteoblast d

ALIGNMENTS

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ID	ABK12137
ABK12137	standard; CDNA; 1321 BP.
AC	ABK12137;
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DT	05-JUN-2002 (first entry)
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DE	Human CDNA encoding Mechanically Induced Vascular Receptor 1, MIVR-1.
XX	
KW	Human; ss; gene; MIVR-1; Mechanically Induced Vascular Receptor 1;
KW	cytostatic; cardiac; cerebroprotective; antiarteriosclerotic;
KW	cardiac cell; anti-apoptotic; vascular endothelial cell;
KW	cardiac hypertrophy; myocardial infarction; stroke; arteriosclerosis;
KW	heart failure.
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OS	Homo sapiens.
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FT	/note= "this region is specifically claimed in claim 3"
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PN	WO200216416-A2.
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PD	28-FEB-2002.
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PF	21-AUG-2001; 2001MO-US26089.
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PR	22-AUG-2000; 2000US-227159P.

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					Gaps
					0:
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QY	361	CG	420		
DB	361	CG	420		
QY	421	CTTGATGGGGGTCAACAGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	480		
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QY	481	GTCGCACTGCAAAAGCGCTTTGTTCCAGAGCATGAGATCAGGAGCTGAGTTGTTCA	540		
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[illegible]

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FT	/tag= b
FT	mat-peptide
FT	90..764
XX	/tag= c
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PN	MO200052022-A1.
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XX	08-SEP-2000.
PR	01-MAR-2000; 2000WO-USO5226.
PA	01-MAR-1999; 99US-0122458.
XX	(MILL-) MILLENNIUM PHARM INC.
PB	Barnes TM, Holtzman DA, Sharp JD, Fraser CC;
PI	WPI: 2000-579269/54.
DR	P-PSDB; AAB18449.
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PT	Novel human and murine secreted proteins designated TANGO 216, 261,
PF	267, 266 and 267 useful as modulating agents of cellular processes,
PP	e.g. for treating cancer -
XX	
PS	Claim 2; Fig 5; 175pp; English.
XX	
CC	The present sequence encodes a human TANGO 261 polypeptide. The
CC	specification also describes TANGO 266, TANGO 216, TANGO 262, and
CC	TANGO 267. The TANGO polypeptides can be used to modulate cellular
CC	proliferation, modulate cellular differentiation and/or modulate
CC	cellular adhesion. The proteins can be used to treat any von Willebrand
CC	factor-associated disorder, regulate extracellular matrix structuring,
CC	cellular adhesion, and cell trafficking and/or migration, modulate
CC	cellular interactions, modulate cell adhesion in proliferative
CC	disorders, such as cancer, modulate the proliferation, differentiation,
CC	and/or function of cells that appear in the bone marrow, and leukocytes,
CC	treat bone marrow, blood and hematopoietic associated diseases and
CC	disorders, osteoarthritis, pulmonary congestion or edema, emphysema,
CC	chronic bronchitis, bronchial asthma and bronchiectasis, intestinal
CC	disorders, spleen associated diseases, modulate renal disorders, treat
CC	cardiovascular disorders such as ischemic heart disease, modulate the
CC	proliferation, differentiation, and/or function of bone and cartilage
CC	cells and to treat bone and/or cartilage associated diseases or
CC	disorder. They may also be used to treat disorders associated with the
CC	ovaries, cerebral oedema, hydrocephalus, brain herniations, iatrogenic
CC	disease, inflammations, bacterial and viral meningitis, Alzheimer's
CC	disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis,
CC	brain cancers, hydrocephalus and encephalitis, and treat hepatic
CC	disorders.
XX	
SQ	Sequence 969 BP; 211 A; 316 C; 294 G; 148 T; 0 other;
Query Match	60.8%; Score 803.2; DB 21; Length 969;
Best Local Similarity	99.6%; Pred. No. 1,9e-120;
Matches 805; Conservative	0; Mismatches 3; Indels 0; Gaps 0
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Db	2 GGAGATGCCGCAGGCTGGAGTTGTTTCAGATCATCATCATCGTGCTGTGATGATGTGAT 61
OY	574 GGTGGTGGTATCACGCTGCTCTGTAGCACTACACAAGCTGTGTGCAGCGCTCTTATCAG 633

Dd		62	GGTGTGTGTATCATCACTGTCGTCGAGCCACTCAAGCTGTCTCGACGGTCTTCAATCA	121
Qy		634	CCGGCACAGCCAGGGGGGGAGAGAGAAGATGCCCTGTCTCAGAAAGATGCCCTGTGGCC	693
Dd		122	CCGGCACAGCCAGGGGGGGAGAGAGAAGATGCCCTGTCTCAGAAAGATGCCCTGTGGCC	181
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Dd		182	CTTCGGAAAGCACTGTCTCAGGCAACGGAAATCCAGAGCCGGAGGTCTACGCCGCCCTCG	241
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Dd		242	GCCCAACGACCGCCTGGGCGGTGGCCCTTGGCCAGGGGGAGGGGCTTCCAGCGCTTCCA	301
Qy		814	GCCCAACCTATCCGTACTCTGCAGCACAGAGATGCAGCTGCACCCACCAATCTTGTCTGAGA	873
Dd		302	GCCCAACCTATCCGTACTCTGCAGCACAGAGATGCAGCTGCAGCCACCAATCTTGTCTGAGA	361
Qy		874	CGGGGAGAGACCCCAACCTTACACAGGGGCCCTGCACCCCTCCAGTTGGGGACCCCGAGCA	933
Dd		362	CGGGGAGAGACCCCAACCTTACACAGGGGCCCTGCACCCCTCCAGTTGGGGACCCCGAGCA	421
Qy		934	GCACCTGGAACTGAACCGGGGAGTGGGTGGCGGCAACCCCAACAGAAACCAATCTTCGACAG	993
Dd		422	GCACCTGGAACTGAACCGGGGAGTGGGTGGCGGCAACCCCAACAGAAACCAATCTTCGACAG	481
Qy		994	TGACCTATGATATGATGTGCACAGCTGGGGGGGCCCTTGCACCCCAAGTAATCTGGGCAT	1053
Dd		482	TGACCTATGATATGATGTGCACAGCTGGGGGGGCCCTTGCACCCCAAGTAATCTGGGCAT	541
Qy		1054	CAGCGCCACAGCTGTACAGGCGACGGCGGGGCGCATGAGAGGGGCGCGCCGCCACCTTACAGCA	1113
Dd		542	CAGCGCCACAGCTGTACAGGCGACGGCGGGGCGCATGAGAGGGGCGCGCCGCCACCTTACAGCA	601
Qy		1114	GGTATATGGCCACTACCCGGGGGTCTCTCTTCACAGACAGAGAGAGAGTGGGGCGCCCTC	1173
Dd		602	GGTATATGGCCACTACCCGGGGGTCTCTCTTCACAGACAGAGAGAGAGTGGGGCGCCCTC	661
Qy		1174	CTTGTCTGAGGGGACCCGGCTCCACACACACACATCGCGCCCTAGAGAGCGAGCCAT	1233
Dd		662	CTTGTCTGAGGGGACCCGGCTCCACACACACACATCGCGCCCTAGAGAGCGAGCCAT	721
Qy		1234	CTGGAGCAAGAGAAAGATTAACAGAAAGACACCCCTCTCTAGAGGTCCCAAGGGGGGCGC	1293
Dd		722	CTGGAGCAAGAGAAAGATTAACAGAAAGACACCCCTCTCTAGAGGTCCCAAGGGGGGCGC	781
Qy		1294	GGCTGGGGCTGCTAGGTGTAAGAAAGGCA 1321	
Dd		782	GGCTGGGGCTGCTAGGTGTAAGAAAGGCA 809	
RESULT 3				
ABK92120				
ID	ABK92120 standard; DNA; 1140 BP.			
XX	('ABK92120;			
DT	15-AUG-2002 (first entry)			
XX	Prostate cancer-associated DNA sequence #6.			
DE	Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;			
XX	gene therapy; gene; ds.			
XX	Mammalia.			
OS	Mammalia.			
XX	WO200230268-A2.			
PN	18-APR-2002.			
XX	12-OCT-2001; 2001WO-US32045.			
PF				
XX				

PR 13-OCT-2000; 2000US-0687576.
 PR 08-DEC-2000; 2000US-0733288.
 PR 08-DEC-2000; 2000US-0733288.
 PR 24-JAN-2001; 2001US-2639579.
 PR 16-MAR-2001; 2001US-2767919.
 PR 16-MAR-2001; 2001US-2768889.
 PR 06-APR-2001; 2001US-2819229.
 PR 24-APR-2001; 2001US-2862149.
 PR 30-APR-2001; 2001US-0847046.
 PR 04-MAY-2001; 2001US-2885899.
 XX
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
 XX
 DR WPI: 2002-471335/50.
 XX
 PT P-PSDB; AB661805.

 Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a prostate tissue -

 XX
 PS Claim 22; Page 305; 436pp; English.
 XX
 CC The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with CC prostate cancer-associated polynucleotides (designated PC genes) that CC selectively hybridize to a sequence that is at least 80% identical CC to them. The prostate cancer-associated polynucleotide sequences CC are differentially expressed in prostate tumour tissue or in CC prostate cancer and are derived from the tissues of various CC organisms such as humans or other mammals (e.g. mice, sheep and dogs). CC The methods of the invention are useful for diagnosing and treating CC prostate cancer in mammals. The prostate cancer-associated genes are CC useful for diagnosing or treating prostate cancer, as well as for CC identifying modulators of prostate cancer or agents that inhibit CC prostate cancer. The nucleic acid sequences are particularly useful CC in gene therapy, as a vaccine or in antisense applications.
 CC
 CC ABR92115-ABR92263 represent prostate cancer-associated polynucleotide CC sequences.
 CC
 SQ Sequence 1140 BP; 270 A; 350 C; 336 G; 184 T; 0 other;

 Query Match 60.7%; Score 802.2; DB 24; Length 1140;
 Best Local Similarity 98.4%; Pred. No. 2,7e-120;
 Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 859 CATCTGCTGTCTCAGACGGGGAGAGACCCACCCTACACAGGCCCTTCACGCT 918
 DB 437 CATCTGCTGTCTCAGACGGGGAGAGACCCACCCTACACAGGCCCTTCACGCT 496
 QY 919 TCGGAGACCCGACAGCAGCTGTGAATGAACCGGAGTGTGTGCGGACCCCAACAG 978
 DB 497 TCGGAGACCCGACAGCAGCTGTGAATGAACCGGAGTGTGTGCGGACCCCAACAG 556
 QY 979 AACCATCTTGACAGTGAATGATAGTGTGACAGCTGGGGGCCCCGCCCCAG 1038
 DB 557 AACCATCTTGACAGTGAATGATAGTGTGACAGCTGGGGGCCCCGCCCCAG 616
 QY 1039 CAGTAACCTCGGCATCAGCCACGCTGTACAGGAGCGGCGCATGAGAGGGCGCC 1098
 DB 617 CAGTAACCTCGGCATCAGCCACGCTGTACAGGAGCGGCGCATGAGAGGGCGCC 676
 QY 1099 GCCCACCCTACAGGAGTGTATGCGCCACTACCCGGGGTCTCTTCAGACACAGAG 1158
 DB 677 GCCCACCCTACAGGAGTGTATGCGCCACTACCCGGGGTCTCTTCAGACACAGAG 736
 QY 1159 CAGTGGGCGCCCTCTGCTGTGAGGGAGCCGCGCTCCACACACATCGCGCCCT 1218
 DB 737 CAGTGGGCGCCCTCTGCTGTGAGGGAGCCGCGCTCCACACACATCGCGCCCT 796
 QY 1219 AGAGAGCGCAGCCATCTGAGAGCAAGAGATTAACAGAAAGACACCCCTCTAGGG 1278
 DB 797 AGAGAGCGCAGCCATCTGAGAGCAAGAGATTAACAGAAAGACACCCCTCTAGGG 856
 QY 1279 TCCCGAGGGGGCGCGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1321
 DB 857 TCCCGAGGGGGCGCGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 899

 RESULT 4
 AAA75163
 ID AAA75163 standard; cDNA; 969 BP.
 AC AAA75163;
 XX
 DT 15-JAN-2001 (first entry)
 XX
 DE cDNA clone encoding a human TANGO 261 polypeptide.
 XX
 KW TANGO 266; TANGO 261; TANGO 262; TANGO 267;
 KW cellular proliferation; cellular differentiation; cellular adhesion;
 KW von Willebrand factor-associated disorder; cell trafficking; cancer;
 KW hematopoietic associated disease; atelectasis; pulmonary congestion;
 KW oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
 KW intestinal disorder; spleen associated disease; renal disorder;
 KW cardiovascular disorder; ischemic heart disease; hydrocephalus;
 KW brain herniation; iatrogenic disease; inflammation; meningitis;
 KW Alzheimer's disease; cerebral toxoplasmosis; Parkinson's disease;
 KW multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 6..764
 FT /tag- a
 FT /product- "TANGO 261"
 XX
 PN WO200052022-A1.
 PD 08-SEP-2000.
 PF 01-MAR-2000; 2000WO-US05226.
 XX
 PR 01-MAR-1999; 99US-0122458.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Barnes TM, Holtzman DA, Sharp JD, Fraser CC;
 XX

DR WPI: 2000-579269/54.
 DR P-PSDB: AAB18461.
 PT Novel human and murine secreted proteins designated TANGO 216, 261,
 PT 262, 266 and 267 useful as modulating agents of cellular processes,
 PT e.g. for treating cancer -
 XX
 PS Disclosure; Page -: 175pp; English.

XX AAA75163-65 encode human TANGO 261 proteins. The specification also
 CC describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO
 CC polypeptides can be used to modulate cellular proliferation, modulate
 CC cellular differentiation and/or modulate cellular adhesion. The
 CC proteins can be used to treat any von Willebrand factor-associated
 CC disorder, regulate extracellular matrix structuring, cellular adhesion,
 CC and cell trafficking and/or migration, modulate cellular interactions,
 CC modulate cell adhesion in proliferative disorders, such as cancer,
 CC modulate the proliferation, differentiation, and/or function of cells
 CC that appear in the bone marrow, and leukocytes, treat bone marrow, blood
 CC and hematopoietic associated diseases and disorders, atelectasis,
 CC pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial
 CC asthma and bronchiectasis, intestinal disorders, spleen associated
 CC diseases, modulate renal disorders, treat cardiovascular disorders such
 CC as ischemic heart disease, modulate the proliferation, differentiation,
 CC and/or function of bone and cartilage cells and to treat bone and/or
 CC cartilage associated diseases or disorder. They may also be used to
 CC treat disorders associated with the ovaries, and cerebral oedema,
 CC hydrocephalus, brain herniations, iatrogenic disease, inflammations,
 CC bacterial and viral meningitis, Alzheimer's disease, cerebral
 CC toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers,
 CC hydrocephalus and encephalitis, and treat hepatic disorders.
 CC note: the present sequence does not appear in the specification; it was
 CC created using information provided.

XX
 XX
 XX Sequence 969 BP: 211 A: 317 C: 293 G: 148 T: 0 other:

Query Match 60.7%; Score 801.6; DB 21; Length 969;
 Best Local Similarity 99.5%; Pred. No. 3.3e-120;
 Matches 804; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 514 GGAGTACGAGGAGGAGTTGTTCATCATCATCATCGGGGAGTGTATGTTAT 573
 DB 2 GGAGTACGAGGAGGAGTTGTTCATCATCATCATCGGGGAGTGTATGTTAT 61
 QY 574 GGTGTGTGTATCAGTGTCTGTGAGCACTACAGTGTGTGACGGTCTTATCAG 633
 DB 62 GGTGTGTGTATCAGTGTCTGTGAGCACTACAGTGTGTGACGGTCTTATCAG 121
 QY 634 CCGGACACGAGGAGGAGGAGAGAGAGATCCCTGTCTCAGAGATGCTGTGGCC 693
 DB 122 CCGGACACGAGGAGGAGGAGAGAGATCCCTGTCTCAGAGATGCTGTGGCC 181
 QY 694 CTGGAGAGCAGAGTGTAGGCAAGGAGATCCAGGCGAGGCTACGCCGCCCTCG 753
 DB 182 CTGGAGAGCAGAGTGTAGGCAAGGAGATCCAGGCGAGGCTACGCCGCCCTCG 241
 QY 754 GCCCAGCAGGCGCTGCGCTGCGCCCTTGCAGGAGGAGGAGGAGGAGGAGGAGG 813
 DB 242 GCCCAGCAGGCGCTGCGCTGCGCCCTTGCAGGAGGAGGAGGAGGAGGAGGAGG 301
 QY 814 GCCCAGCAGTGTGTATCAGTGTCTGTGAGCACTACAGTGTGTGACGGTCTTATCAG 873
 DB 302 GCCCAGCAGTGTGTATCAGTGTCTGTGAGCACTACAGTGTGTGACGGTCTTATCAG 361
 QY 874 CGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 933
 DB 362 CGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 421
 QY 934 GCAGCTGGAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 993
 DB 422 GCAGCTGGAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 481
 QY 994 TGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1053

DB 482 TGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 541
 QY 1054 CAGCGCCAGCTGTCTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1113
 DB 542 CAGCGCCAGCTGTCTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 601
 QY 1114 GGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1173
 DB 602 GGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 661
 QY 1174 CTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1233
 DB 662 CTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 721
 QY 1234 CTGGAGCAAGAGAGAGATTAACAGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 1293
 DB 722 CTGGAGCAAGAGAGAGATTAACAGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 781
 QY 1294 GGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1321
 DB 782 GGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 809

RESULT 5
 AAA75164
 ID AAA75164 standard; cDNA; 969 BP.
 XX
 XX AAA75164;
 AC
 XX 15-JAN-2001 (first entry)
 DT
 XX
 XX cDNA clone encoding a human TANGO 261 polypeptide.

XX TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267;
 KW cellular proliferation; cellular differentiation; cellular adhesion;
 KW von Willebrand factor-associated disorder; cell trafficking; cancer;
 KW hematopoietic associated disease; atelectasis; pulmonary congestion;
 KW oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
 KW intestinal disorder; spleen associated disease; renal disorder;
 KW cardiovascular disorder; ischemic heart disease; hydrocephalus;
 KW brain herniation; iatrogenic disease; inflammation; meningitis;
 KW Alzheimer's disease; cerebral toxoplasmosis; Parkinson's disease;
 KW multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.

OS Homo sapiens.
 FH
 FH Key Location/Qualifiers
 FT CDS 6..764
 FT /tag- a
 FT /product- "TANGO 261"

PN WO200052022-A1.

XX 08-SEP-2000.

PD 01-MAR-2000; 2000MO-US05226.

PF 01-MAR-1999; 99US-0122458.

XX (MILL-) MILLENNIUM PHARM INC.

PA Barnes TM, Holtzman DA, Sharp JD, Fraser CC;

PI WPI: 2000-579269/54.

XX P-PSDB: AAB18462.

DR Novel human and murine secreted proteins designated TANGO 216, 261,
 PT 262, 266 and 267 useful as modulating agents of cellular processes,
 PT e.g. for treating cancer -

XX Disclosure; Page -: 175pp; English.

CC AAA75163-65 encode human TANGO 261 proteins. The specification also
 CC describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO
 CC polypeptides can be used to modulate cellular proliferation, modulate
 CC cellular differentiation and/or modulate cellular adhesion. The
 CC proteins can be used to treat any von Willebrand factor-associated
 CC disorder, regulate extracellular matrix structuring, cellular adhesion,
 CC and cell trafficking and/or migration, modulate cellular interactions,
 CC modulate cell adhesion in proliferative disorders, such as cancer,
 CC modulate the proliferation, differentiation, and/or function of cells
 CC that appear in the bone marrow, and leukocytes, treat bone marrow, blood
 CC and hematopoietic associated diseases and disorders, atelectasis,
 CC pulmonary congestion or edema, emphysema, chronic bronchitis, bronchial
 CC asthma and bronchiectasis, intestinal disorders, spleen associated
 CC diseases, modulate renal disorders, treat cardiovascular disorders such
 CC as ischemic heart disease, modulate the proliferation, differentiation,
 CC and/or function of bone and cartilage cells and to treat bone and/or
 CC cartilage associated diseases or disorder. They may also be used to
 CC treat disorders associated with the ovaries, and cerebral edema,
 CC hydrocephalus, brain herniations, latrogenic disease, inflammations,
 CC bacterial and viral meningitis, Alzheimer's disease, cerebral
 CC toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers,
 CC hydrocephalus and encephalitis, and treat hepatic disorders.
 CC note: the present sequence does not appear in the specification; it was
 CC created using information provided.

XX Sequence 969 BP; 210 A; 317 C; 294 G; 148 T; 0 other:

Query Match 60.7%; Score 801.6; DB 21; Length 969;
 Best Local Similarity 99.5%; Pred. No. 3.3e-120;
 Matches 804; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

514 GGAGATACGAGAGGCTGGAGTTGTTTCAGATCATCATCGTGTGTGATGATGTGAT 573
 2 GGAGATGCGGAGCTGAGTTGTTTCAGATCATCATCGTGTGTGATGATGTGAT 61
 574 GGTGGTGTGATACAGTGTCTGTCAGCCACTACAGCTGTCTGACAGGCTCTTCATCAG 633
 62 GGTGGTGTGATACAGTGTCTGTCAGCCACTACAGCTGTCTGACAGGCTCTTCATCAG 121
 634 CCGGACACGAGGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 693
 122 CCGGACACGAGGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181
 694 CTCGAGAGACACAGTGTGAGGCAACGAGATCCACAGAGCCGACAGGTCTACGCCGCTCG 753
 182 CTCGAGAGACACAGTGTGAGGCAACGAGATCCACAGAGCCGACAGGTCTACGCCGCTCG 241
 754 GCCCACCAGCGCCCTGGCGCGCGCCCTTGCCCGCAGGCGGAGGAGGAGGAGGAGGAG 813
 242 GCCCACCAGCGCCCTGGCGCGCGCCCTTGCCCGCAGGCGGAGGAGGAGGAGGAGGAG 301
 814 GCCCACCATCTGCTGCTGACAGCAGAGATGAGCTGACCCACCCACCATCTGCTGTGAGA 873
 302 GCCCACCATCTGCTGCTGACAGCAGAGATGAGCTGACCCACCCACCATCTGCTGTGAGA 361
 874 CCGGAG 933
 362 CCGGAG 421
 934 GGAGCGGAAGTGAACCGGAGAGTGTGTGCGCAGCCCAACAGAACATCTTGAGAGAG 993
 422 GGAGCGGAAGTGAACCGGAGAGTGTGTGCGCAGCCCAACAGAACATCTTGAGAGAG 481
 994 TGACCTGATGATAGTGTGAGGCTGGGCGGCGCCCTTGCCCGCAGAGATGATCTGGGCAT 1053
 482 TGACCTGATGATAGTGTGAGGCTGGGCGGCGCCCTTGCCCGCAGAGATGATCTGGGCAT 541
 1054 CAGCGCCACAGTGTGAGGAGAGGCGGCGGAGTGAAGGAGGAGGAGGAGGAGGAGGAG 1113
 542 CAGCGCCACAGTGTGAGGAGAGGCGGCGGAGTGAAGGAGGAGGAGGAGGAGGAGGAG 601
 1114 GGTCATGCGGACATACCGGCGGAGTCTCTTCAGACACAGAGAGAGAGAGAGAGAGAGAG 1173

Db 602 GGTATGCGCCACATACCGGCGGCTCTCTTCACAGCAGCAGAGAGAGAGAGAGAGAG 661
 QY 1174 CTGTGTGAGAGGAG 1233
 Db 662 CTGTGTGAGAGGAG 721
 QY 1234 CTGTGTGAGAGGAG 1293
 Db 722 CTGTGTGAGAGGAG 781
 QY 1294 GGTGTGAGAGGAG 1353
 Db 782 GGTGTGAGAGGAG 841

RESULT 6

AAA75165
 ID AAA75165 standard; cDNA; 969 BP.

AAA75165;

15-JUN-2001 (first entry)

cDNA clone encoding a human TANGO 261 polypeptide.

TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267;
 cellular proliferation; cellular differentiation; cellular adhesion;
 von Willebrand factor-associated disorder; cell trafficking; cancer;
 hematopoietic associated disease; atelectasis; pulmonary congestion;
 edema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
 intestinal disorder; spleen associated disease; renal disorder;
 cardiovascular disorder; ischemic heart disease; hydrocephalus;
 brain herniation; latrogenic disease; inflammation; meningitis;
 Alzheimer's disease; cerebral toxoplasmosis; Parkinson's disease;
 multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.

XX Homo sapiens.

XX Location/Qualifiers

XX Key

XX CDS

/*tag- a
 /product- "TANGO 261"

XX WO200052022-A1.

XX 08-SEP-2000.

XX 01-MAR-2000; 2000WO-US05226.

XX 01-MAR-1999; 99US-0122458.

XX (MILL-) MILLENNIUM PHARM INC.

XX Barnes TM, Holtzman DA, Sharp JD, Fraser CC;

XX WPI; 2000-579269/54.

XX P-PSDB; AAB18463.

XX Novel human and murine secreted proteins designated TANGO 216, 261,

XX e.g. for treating cancer -

XX Disclosure; Page -: 175pp; English.

CC AAA75163-65 encode human TANGO 261 proteins. The specification also
 CC describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO
 CC polypeptides can be used to modulate cellular proliferation, modulate
 CC cellular differentiation and/or modulate cellular adhesion. The
 CC proteins can be used to treat any von Willebrand factor-associated
 CC disorder, regulate extracellular matrix structuring, cellular adhesion,
 CC and cell trafficking and/or migration, modulate cellular interactions,
 CC modulate the proliferation, differentiation, and/or function of cells

CC that appear in the bone marrow, and leukocytes treat bone marrow, blood
CC and hematopoietic associated diseases and disorders, atelactasis,
CC pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial
CC asthma and bronchiectasis, intestinal disorders, spleen associated
CC diseases, modulate renal disorders, treat cardiovascular disorders such
CC as ischemic heart disease, modulate the proliferation, differentiation,
CC or/and function of bone and cartilage cells and to treat bone and/or
CC cartilage associated diseases or disorder. They may also be used to
CC treat disorders associated with the ovaries, and cerebral oedema,
CC hydrocephalus, brain herniations, iatrogenic disease, inflammations,
CC bacterial and viral meningitis, Alzheimer's disease, cerebral
CC toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers,
CC hydrocephalus and encephalitis, and treat hepatic disorders.
CC note: the present sequence does not appear in the specification; it was
CC created using information provided.

SD Sequence 969 BP; 210 A; 317 C; 294 G; 148 T; 0 other;

Query Match	60.78%	Score	801.6	DB	21	Length	969
Best Local Similarity	99.58%	Pred. No.	3,3e-120				
atches 804; Conservative	0	Mismatches	4	Indels	0	Gaps	0

QY	514	GGAGTATCAACGAGCGGAGGTTGGTTGGTTCACATATATCATACATCCGCGGGGGGATGATGATGATG	573
Dp	2	GGAGATGGCGGAGCGTGGAGTTTGTTCATATCATATCATATCGGGGGGTGATGATGATGATG	61
QY	574	GGTGGTGGTGCATCACTGCTGCTGAGCCACTACAAAGCTGHTGTGCACGGTCCCTTATCAG	633
Dp	62	GGTGGTGGTGCATCACTGCTGCTGAGCCACTACAAAGCTGHTGTGCACGGTCCCTTATCAG	121
QY	634	CCGGCACAGCCAGGGGGCGGAGAGAGAAATGCTCTGTCTTCAGAAAGATGCTGTGGCC	693
Dp	122	CCGGCACAGCCAGGGGGCGGAGAGAGAAATGCTCTGTCTTCAGAAAGATGCTGTGGCC	181
QY	694	CTGGAGAGGACAGAGTGCAGGCAACGGAAATCCAGAGCCGAGAGTCAAGGCCCGCGCTCG	753
Dp	182	CTGGAGAGGACAGAGTGCAGGCAACGGAAATCCAGAGCCGAGAGTCAAGGCCCGCGCTCG	241
QY	754	GCCCAACCGACCGCTGGGCCGTGGCCCTTGTGGCCAGCGGAGAGCGACTTCCACCGGTGCCA	813
Dp	242	GCCCAACCGACCGCTGGGCCGTGGGCCCTTGTGGCCAGCGGAGAGCGACTTCCACCGGTGCCA	301
QY	814	GCCCAACCTATCCGTACTGTGCAGACACGAAATGCACTGCCACCCACCATCTCGCTGTCA	873
Dp	302	GCCCAACCTATCCGTACTGTGCAGACACGAAATGCACTGCCACCCACCATCTCGCTGTCA	361
QY	874	CGGGGAGAGGAGCCCGCACCCCTTGCACAGGGGCCCTTGCACCCCTTGCAGGTTCCGGAGACCCGAGCA	933
Dp	362	CGGGGAGAGGAGCCCGCACCCCTTGCACAGGGGCCCTTGCACCCCTTGCAGGTTCCGGAGACCCGAGCA	421
QY	934	GCAGCTGGAATGAAACCGGAGGTGCTGTCGGCACCCACCCCAACAGAACCATCTTGCACAG	993
Dp	422	GCAGCTGGAATGAAACCGGAGGTGCTGTCGGCACCCACCCCAACAGAACCATCTTGCACAG	481
QY	994	TGACCTGATGATGATGCTGCCAGGCTGTGGGGCCCTTGGCCCCCAGACAGTAACTCGGGCAT	1053
Dp	482	TGACCTGATGATGATGCTGCCAGGCTGTGGGGCCCTTGGCCCCCAGACAGTAACTCGGGCAT	541
QY	1054	CAGGCGCCACGTCCTACGGCAGCGGGGGGGCGCATGGAGGGGGCGCGGCCACCACTTAAGAGCA	1113
Dp	542	CAGGCGCCACGTCCTACGGCAGCGGGGGGGCGCATGGAGGGGGCGCGGCCACCACTTAAGAGCA	601
QY	1114	GGTCATCGGCGCACTTACCCCGGGGTCTCTCTCCAGCAGCAGCAGCAGTGGGCGCGCCCTC	1173
Dp	602	GGTCATCGGCGCACTTACCCCGGGGTCTCTCTCCAGCAGCAGCAGCAGTGGGCGCGCCCTC	661
QY	1174	CTTGCTGGAGGGGAGCCGGCTTCACACACACATCGGGCCCTTAAGAGCGCAGCCAT	1233
Dp	662	CTTGCTGGAGGGGAGCCGGCTTCACACACACATCGGGCCCTTAAGAGCGCAGCCAT	721
QY	1234	CTGGAGCAAGAGGAAGATTAACAAAGAAAGAACACCTCTCTTGGGGTCCCCAGGGGGGGCG	1293
Dp	722	CTGGAGCAAGAGGAAGATTAACAAAGAAAGAACACCTCTCTTGGGGTCCCCAGGGGGGGCG	781

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QY      1294 GGCTGGGGCTGCGTAGGTGAAAAGGCAG 1321
          |||||
Db      782  GGCTGGGGCTGCGTAGGTGAAAAGGCAG 809

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RESULT 7
AAAA7429
ID   AAA47429 standard; DNA; 1061 BP.

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AC AAA47429

DT 20-OCT-2000 (first entry)

Sequence encoding human neuron-associated protein

KM Neuron associated protein; NEAP; neurological disorder; epilepsy;
KM ischemic cerebrovascular disease; stroke; cerebral neoplasm;
KM Alzheimer's disease; Pick's disease; Huntington's disease;
KM dementia; Parkinson's disease; demyelinating disease; meningitis;
KM prion disease; kuru; Creutzfeldt-Jakob disease; neurofibromatosis;
KM cerebral palsy; muscular dystrophy; central nervous system; CNS;
KM peripheral nervous system; PNS; myopathy; schizophrrenia;
KM acinic keratosis; arteriosclerosis; atherosclerosis; burstitts;
KM chorioid; hepatitis; mixed connective tissue disease; MCTD;
KM myelofibrosis; paroxysmal nocturnal haemoglobinuria; cancer;
KM autoimmune disease; inflammation; acquired immunodeficiency syndrome;
KM AIDS; Addison's disease; adult respiratory distress syndrome;
KM allergy; ankylosing spondylitis; amyloidosis; anaemia; asthma;
KM Werner syndrome; trauma; human; ds.

OS Homo sapiens.

Key	Location/Qualifiers
FH	101..859
FT	/*tag= a
FT	/product= Neuron associated protein
FT	

PD 15-JUN-2000.

PF 10-DEC-1999; 99WO-US30408.

11-DEC-1998 094115-0210083
XX
PR

PR	11-DEC-1998;	98US-9123456.
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PR 09-FEB-1999; 99US-0119365.

PR 16-MAR-1999; 99DS-0124687.
YY

PA (INCY-) INCYTE PHARM INC.

PI Tang YT, Yue H, Baughn MR, Hillman JL, Lai P, Au-young J, Yang J;
PI Lu DAM, Azimzal Y;

DR WPI; 2000-423423/36
DR P-PSDB; AAB01388.

PT New human neuron-associated proteins and polynucleotides encoding them,
 PT useful for diagnosis, treatment and prevention of cell proliferative
 PT disorders including cancer, neuronal and neurological disorders
 XX
 PS Claim 9; Page 136; 145pp; English.

PS Claim 9; Page 136; 145pp; English.

CC Human neuron-associated proteins (NEUAP) can be used for
CC treating or preventing a disorder associated with decreased
CC expression or activity of NEUAP. Antagonists of NEUAP are useful for
CC treating or preventing disorder associated with increased expression
CC or activity of NEUAP. NEUAP or their fragments or derivatives are
CC useful for treating neurological disorder such as epilepsy, ischemic
CC cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's
CC disease, Pick's disease, Huntington's disease, dementia and
CC Parkinson's disease. NEUAPs are also useful for treating other
CC demyelinating diseases, bacterial and viral meningitis, prion

CC disease including kuru, Creutzfeldt-Jakob disease, nutritional and
CC metabolic diseases of the nervous system, neurofibromatosis, other
CC developmental disorders of the central nervous system, cerebral
CC palsy, neuroskeletal disorders, autonomic nervous system disorders,
CC cranial nerve disorders, spinal cord diseases, muscular dystrophy and
CC other neuromuscular disorders, peripheral nervous system disorders,
CC inherited, metabolic, endocrine, and toxic myopathies, mental
CC disorders including mood, anxiety and schizophrenic disorders, a cell
CC proliferative disorder such as actinic keratosis, arteriosclerosis,
CC atherosclerosis, burditts, cirrhosis, hepatitis, mixed connective
CC tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal
CC hemoglobinuria, cancers of the adrenal gland, bladder, bone,
CC bone marrow, brain, breast, cervix, and an autoimmune/inflammatory
CC disorder such as acquired immunodeficiency syndrome (AIDS), Addison's
CC disease, adult respiratory distress syndrome, allergies, ankylosing
CC spondylitis, amyloidosis, anemia, asthma, Werner syndrome,
CC complications of cancer, hemodialysis, and extracorporeal circulation
CC viral, bacterial, fungal, parasitic, protozoal, and hematologic
CC infections, and trauma. This sequence was given the InCite ID no.
1871288CBL.

Sequence 1061 BP; 225 A; 342 C; 326 G; 168 T; 0 other;

Query Match	60.68	Score 800.6	DB 21	Length 1061

Best Local Similarity 98.3%; Pred. No. 4.8e-120;

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Matches 809; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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[illegible]

Db 742 CAGTGGGGCCGCCCTCCTTCTGTGGAGGGAGCCGGGCTCCACACACACATCGGGGCCCTT 801

Q7 1219 AGAGACGCGACGCATCTGTGAGCAAAAGAMGGATTTAAAGAAAGAGACCCCTCTTAGG 127

Db 802 AGAGAGCGCAGCCATCTTGGAGCAAGAGAGAGATTAACAGAAAGACACCCCTCTTAGG 861

Q7 1279 TCCCCAGGGGGGCCGGGCTGGGGCTGCGTAGGTGAAAAAGCGAG 1321

Db 862 TCCCCAAGGGGGGCCGGGCTGGGGCTGCGTAGGTGAAAAAGCGAG 904

RESULT 8

ID ABZ36103 standard; cDNA; 1334 BP.

AC ABZ36103

DT 10-FEB-2003 (first entry)

DE Human secretory polynucleotide SPTM SEQ ID NO 267.

KM Human; SPTM: autoimmune disorder; inflammatory disorder; AIDS; anaemia
KM asthma; disease; neurological disorder; epilepsy; cancer;
KM Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;
KM multiple sclerosis; Parkinson's disease; cell proliferative disorder;
KM anti-inflammatory; immunosuppressive; neuroprotective; nootropic;
KM neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic;
KM antipsychotic; antinausea; anti-HIV; human immunodeficiency virus;
KM secretory polynucleotide; secretory protein; gene; ss.

OS Homo sapiens.

PN WO200283876-A2

PD 24-OCT-2002

PF 27-MAR-2002; 2002WO-US09921.

PR 29-MAR-2001; 2001US-2800667
PR 29-MAR-2001; 2001US-2800687
PR 15-MAY-2001; 2001US-291280P
PR 17-MAY-2001; 2001US-291829P
PR 17-MAY-2001; 2001US-291849P
PR 19-JUN-2001; 2001US-299428P
PR 19-JUN-2001; 2001US-299776P
PR 20-JUN-2001; 2001US-300001P

PA (INCY-) INCYTE GENOMICS INC.

PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen B, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tusson O, Yap PP,
PI Daugherty SC, Dam TC, Liu TP, Nguyen DA, Kleefeld Y, Gerstein EH
PI Peraltta CH, Daulton MH, Lewis SA, Chen AJ, Panzer SR, Harris B,
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
xx
WPI: 2003-075543/07.
DR P-PSDB: ABP755660.

xx New human secretory proteins and polynucleotides, useful for
 pt diagnosing, treating or preventing autoimmune/inflammatory disorders
 pt (e.g. AIDS), neurological disorders (e.g. Alzheimer's), or cell
 pt proliferations or cancers -

PS Claim 1; SEQ ID NO 267; 458bp + Sequence Listing; English.

The invention relates to a secretory polynucleotide (designated spm) comprising any of 567 polynucleotide sequences (AB335837-AB336403), a naturally occurring polynucleotide sequence at least 90% identical to the polynucleotide sequence, a polynucleotide complementary to them or an RNA equivalent of them. The polypeptide or polynucleotide are useful for treating, preventing or diagnosing a disease or condition associated with the expression of functional SPM. These are particularly useful for diagnosing, treating or preventing autoimmune/inflammatory disorders

Db 708 GGGCGTGGCCGCTTCCGCGAGCGGAGCGCTTCCAGCCGCTTCCAGCCGCTATCCGTA 649
 Qy 829 CCTGAGCAGAGATGACAGCTGCGACACCCACATCTGCTGTCAGAGCGGAGAGAGCCCC 888
 Db 648 CCTGAGCAGAGATGACAGCTGCGCGCCACTATTTGCTGTCAGAGCGGAGAGAGCCCC 589
 Qy 889 ACCCTACAGAGCGGCGCTGACCTTCAGCTTCGGAGCCGAGCAGCAGCTGGAATGAA 948
 Db 588 ACCCTACAGAGCGGCGCTGACCTTCAGCTTCGGAGCCGAGCAGCAGCTGGAATGAA 529
 Qy 949 CCGGAGTGGTGGCGGCGACCCCAACAGAACCATCTTCGAGTGTACTGATGATGATG 1008
 Db 528 CCGGAGTGGTGGCGGCGACCCCAACAGAACCATCTTCGAGTGTACTGATGATGATG 469
 Qy 1009 TGGCAGGCTGGGCGGCGGCTGCGCGCGCGAGAGTAACTGGGAGCAGCGCAGCTGCTA 1068
 Db 468 TGGCAGGCTGGGCGGCGGCTGCGCGCGAGAGTAACTGGGAGCAGCGCAGCTGCTA 409
 Qy 1069 CGGAGCGGCGGCGGCGGAGAGGCGCGCG -CCGACTTACAGCGAGTCAATCGGCGACT 1127
 Qy 408 CGGAGCGGCGGCGGCGGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 349
 Qy 1128 ACCGCGGCTGCTCTCTCCAGCAGCAGAGAGAGTGGGCGCGCGCTCTGCTGGAGGGGA 1187
 Db 348 ACCGCGGCTGCTCTCTCCAGCAGCAGAGAGAGTGGGCGCGCGCTCTGCTGGAGGGGA 289
 Qy 1188 CCGGCGCTCCACACACACATCGCGCGCGCTAGAGAGCGCAGCGCATCTGAGCAAGAGA 1247
 Db 288 CCGGCGCTCCACACACACATCGCGCGCGCTAGAGAGCGCAGCGCATCTGAGCAAGAGA 229
 Qy 1248 AGGATAAACAGAAAGAGACCTCTCTAGGGTCCCGAGGGGGCGCGGCTGGGCTGGCT 1307
 Db 228 AGGATAAACAGAAAGAGACCTCTCTAGGGTCCCGAGGGGGCGCGGCTGGGCTGGCT 169
 Qy 1308 AGTGAAAAAGGCGAG 1321
 Db 168 AGTGAAAAAGGCGAG 155
 RESULT 11
 ABR12142
 ID ABR12142 standard; cDNA; 878 BP.
 AC ABR12142;
 DT 05-JUN-2002 (first entry)
 DE Mouse cDNA encoding Mechanically Induced Vascular Receptor 1, MIVR-1.
 KW Mouse; ss; gene; MIVR-1; Mechanically Induced Vascular Receptor 1;
 KW cytoskeletal; cardiant; cerebroprotective; antiarteriosclerotic;
 KW cardiac cell; anti-apoptotic; vascular endothelial cell;
 KW cardiac hypertrophy; myocardial infarction; stroke; arteriosclerosis;
 KW heart failure.
 OS Mus musculus.
 FT Key Location/Qualifiers
 FT CDS 20..844
 FT /tag- a
 FT /product- "MIVR-1"
 PN WO200216416-A2.
 PD 28-FEB-2002.
 PF 21-AUG-2001; 2001WO-US26089.
 PR 22-AUG-2000; 2000US-227159P.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 PA (PFI) PFIZER INC.
 XX

PI Lee RT, Landschulz KT, Kennedy SP, Thompson JF, Turf TG;
 DR WPI; 2002-280912/32.
 DR P-PSDB; AAV78236.
 PT Novel nucleic acid molecule encoding Mechanically Induced Vascular
 PT Receptor-1 polypeptide, useful for treating cardiovascular diseases -
 XX
 PS Disclosure; Page 99-100; 105pp; English.
 CC The invention relates to an isolated nucleic acid molecule encoding a
 CC Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having
 CC cardiac cell anti-apoptotic activity and fragments of it provided
 CC they are not identical to Genbank sequences A176144.1, A1594390,
 CC NM_004338 and A0177461. Also included are expression vectors, host
 CC cells, the MIVR-1 polypeptide, MIVR-1 binding peptides, modulators of
 CC MIVR-1, contacting a molecule having cardiac cell anti-apoptotic activity
 CC with a candidate agent, where the molecule is a nucleic acid molecule
 CC comprising MIVR-1, IEX-1, VDUP-1, BTG-2 and TIS-11d or its
 CC expression product, determining if the anti-apoptotic activity is
 CC modulated and thereby identifying a modulator. The cardiac cell anti-
 CC apoptotic molecules and nucleic acids of the invention are useful for
 CC treating, diagnosing and monitoring progression of such diseases and
 CC disorders as characterized by increased apoptotic cell-death of vascular
 CC endothelial cells e.g. cardiac hypertrophy, myocardial infarction,
 CC stroke, arteriosclerosis and heart failure. The present sequence
 CC encodes mouse MIVR-1.
 CC
 SQ Sequence 878 BP; 179 A; 305 C; 247 G; 147 T; 0 other;
 Query Match 46.7%; Score 616.4; DB 24; Length 878;
 Best Local Similarity 84.3%; Pred. No. 1.8e-90;
 Matches 740; Conservative 0; Mismatches 111; Indels 27; Gaps 3;
 Qy 416 CACGCGTGTAGGGGGGTCAACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 475
 Db 11 CATGGCTGATGGGGGTCAACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 70
 Qy 476 TGCAGTGCACACTGCAAAAGCTCTTGTTCAGAGCATGAGATCAGGAGCTGAGTTT 535
 Db 71 TGGCGGTGAACACTGCGACGGCTTGTTCAGAGCATGAGATCAGGAGCTGAGTTT 130
 Qy 536 GTTCAGATCATCATCATGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 595
 Db 131 GTGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 190
 Qy 596 CTGAGCCACTACAACTGCTGTCAGAGGCTTCATCAGCGCGGACAGCGAGGGGGAGG 655
 Db 191 CTGAGCCACTACAACTGCTGTCAGAGGCTTCATCAGCGCGGACAGCGAGGGGGAGG 250
 Qy 656 AGAGAGATGAGCTGCTCAGAGAGATGAGCTGAGCGCTGAGAGAGCAGATGTCAGGC 715
 Db 251 AGAGAGATGAGCTGCTCAGAGAGATGAGCTGAGCGCTGAGAGAGCAGATGTCAGGC 309
 Qy 716 AAGGAATCCAGAGCGCGAGGTACGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGTG 775
 Db 310 --TGGAATGCGGAGCCAGAGGTATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTG 367
 Qy 776 CCGCGCTTGGCGGAGGAGGCTTCACGCGCTTCAGCGCGCGCGCGCGCGCGCGCGCGCGTG 835
 Db 368 CCGCGCTTGGCGGAGGAGGCTTCACGCGCTTCAGCGCGCGCGCGCGCGCGCGCGCGCGTG 418
 Qy 836 CAGGAGATGAGCTGCTCAGAGAGATGAGCTGAGCGCGGAGAGAGCGCGCGCGCGCGCGTG 895
 Db 419 CAGGAGATGAGCTGCTCAGAGAGATGAGCTGAGCGCGGAGAGAGCGCGCGCGCGCGCGTG 478
 Qy 896 CAGGCG 955
 Db 479 CAGGCG 538
 Qy 956 TCGGTGCGGCG 1015
 Db 539 TCGGTGCGGCG 598

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 27, 2003, 17:43:55 ; Search time 3107 seconds

(without alignments)
10333.509 Million cell updates/sec

Title: US-09-934-249-1

Perfect score: 1321

Sequence: 1 cgaccgcggtctcgagcga.....ctgcgtaggtgaaagcag 1321

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 segs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_liv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	866	65.6	1201	9	AL517150
C 2	859.4	65.1	1009	9	AL578575
C 3	766.8	58.0	967	13	BM641849
C 4	766	58.0	1046	12	BM922276

Result No.	Score	Query Match	Length	ID	Description
5	764.2	57.9	1201	9	AL543170
6	736.4	55.7	916	13	BQ954555
C 7	735	55.6	951	9	AL558881
C 8	715.4	54.2	1007	9	AL558882
C 9	715	54.1	874	13	BX362396
10	691.2	52.3	945	13	BQ539219
11	686.6	52.0	850	13	BQ602918
12	630.6	47.7	1207	11	AK008976
13	618.6	46.8	1079	11	BC023092
C 14	614.6	46.5	782	12	BQ015170
15	607.4	46.0	609	13	BQ636742
16	605.8	45.9	915	13	BX344441
17	592	44.8	888	13	BX362397
18	578.4	43.8	890	13	BQ690750
19	570.4	43.2	973	13	BQ169156
C 20	567.4	43.0	729	13	BQ575741
C 21	564.8	42.8	730	12	BM677602
C 22	563.2	42.6	728	12	BM683523
23	550	41.6	551	12	BM141979
24	529.8	40.1	894	12	B1851941
25	521	39.4	1068	13	BQ527705
26	501.6	38.0	588	12	BM483503
C 27	493.6	37.4	693	9	A1761441
28	493.4	37.4	655	13	BQ691705
29	486	36.8	1400	12	BM559329
30	480.8	36.4	964	13	BQ859860
31	478.6	36.2	1174	9	AL517151
32	477.6	36.2	646	13	BQ859841
33	476.4	36.1	651	14	CB554226
34	473.4	35.8	1017	13	BX400248
35	468.8	35.5	1280	13	BQ691500
36	468	35.4	857	10	BQ323347
C 37	468	35.3	744	10	BM624904
C 38	465.8	35.3	744	13	BQ414421
C 39	461	34.9	763	12	B1646175
C 40	455.4	34.5	629	13	BQ730650
C 41	453.4	34.3	949	13	BX365486
C 42	452.2	34.2	618	14	CD367193
C 43	448	33.9	626	12	BM974296
C 44	444.2	33.6	990	13	BQ691066
C 45	442	33.5	602	14	CA431191

ALIGNMENTS

RESULT 1
AL517150/c
LOCUS
DEFINITION
CSODA008YB23 3-PRIME, mRNA sequence.
ACCESSION
AL517150
VERSION
AL517150.2
KEYWORDS
GI:30492472
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 1201)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Li, W.-B., Gruber, C., Jessee, J. and Polyes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12780643.
COMMENT
Contact: Genoscope
Genoscope, Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9945.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CSODA008CA12NP1&cluster=9945.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DA008CA12NP1.
Location/Qualifiers

FEATURES

source

1. 1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DA008B23"
/issue_type="NEUROBLASTOMA"
/clone_1lb="Homo sapiens NEUROBLASTOMA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
BASE COUNT 177 a 372 c 401 g 214 t 37 others
ORIGIN

Query Match

Best Local Similarity 88.9%; Pred. No. 2.1e-142;
Matches 926; Conservative 23; Mismatches 91; Indels 2; Gaps 2;

280 GCCCGGCGAGCGGGGCGCGCTCCCGCGCGCGCTCCTGCATGCGGGGCGCCCACT 339
1157 SCCCGSGCCCGGTTTMSGGCCCGGSGCGGGGCGGCTTCCCGCGGCTCBGG 1098
340 CCGGGCG 399
1097 TKGGGGCGCGGTCGGGGGGRGASCCCMCGMAAAMAAAAAMAAAMCSRMNAAGGC 1058
400 CGCGCGCGCGCTGCATGCAACGCTTGATGGGGGTAAACAGACCGCGCGCGCGCG 459
1037 CGCCSGCGCGCTGCATGCAACGCTTGATGGGGGTAAACAGACCGCGCGCGCGCG 979
460 GCAGCCCAATCTCTCTGACAGTCAACGCTCTTGTTCAGAGCATGAGAT 519
978 GCACCCCAATCTCTCTGACAGTCAACGCTCTTGTTCAGAGCATGAGAT 919
520 CAGGAGGTGAGTTTGTTCAGATCATCATGCTGTGTATGATGATGATGATGATG 579
918 CAGGAGGTGAGTTTGTTCAGATCATCATGCTGTGTATGATGATGATGATGATG 859
580 GGTGATCAGTCCCTGCTGAGCCACTAAGCTGTGTGACAGCGCTTCATCAGCGCG 639
858 GGTGATCAGTCCCTGCTGAGCCACTAAGCTGTGTGACAGCGCTTCATCAGCGCG 799
640 CAGGAGGTGAGTTTGTTCAGATCATCATGCTGTGTATGATGATGATGATGATG 699
798 CAGGAGGTGAGTTTGTTCAGATCATCATGCTGTGTATGATGATGATGATGATG 739
700 GAGCAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 759
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760 GAGCAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 819
679 GAGCAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 620
820 CTATCGTACTCTGACAGAGATGCACTGCCACCACTCTGCTGTGACAGCGGGA 879
619 CTATCGTACTCTGACAGAGATGCACTGCCACCACTCTGCTGTGACAGCGGGA 560
880 GAGCAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 939
559 GAGCAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 500
940 GGAATGAAACGGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 999
499 GGAATGAAACGGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 440
1000 GATGATATGTCAGAGCTGGGGGCGCGCTTCCCGCGCGCGCGCGCGCGCGCGCG 1059
439 GATGATATGTCAGAGCTGGGGGCGCGCTTCCCGCGCGCGCGCGCGCGCGCGCG 380

1060 CACGTCTACGCGAGCG 1119
379 CACGTCTACGCGAGCG 320
1120 CGGCGACACCG 1179
319 CGGCGACACCG 260
1180 GGAAGGAGCG 1239
259 GGAAGGAGCG 200
1240 CAAGAGAGAGTAAACAGAAAGACACCTCTCTAGAGTCCCGAGGCGCGCGCGCG 1299
199 CAAGAGAGAGTAAACAGAAAGACACCTCTCTAGAGTCCCGAGGCGCGCGCGCG 140
1300 GGCTGCTAGGTGAAAGGCGAG 1321
139 GGCTGCTAGGTGAAAGGCGAG 118

RESULT 2
AL578575/c 1009 bp mRNA linear EST 01-JUN-2003
LOCUS
DEFINITION
AL578575 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
ACCESSION
AL578575
VERSION
AL578575.2 GI:31316780
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
1 (Phases 1 to 1009)
AUTHORS
Ll, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished
COMMENT
On Feb 16, 2001 this sequence version replaced gi:12942781.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9945.r for
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DK001B12NP1&cluster=9945.r. Contact :
Feng Liang Email : fliang@life.techn.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DK001B12NP1.

FEATURES

source

1. 1009
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/mol_type="mRNA"
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/clone="CS0DK001YC24"
/cell_type="HELA CELLS COT 25-NORMALIZED"
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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 160 a 293 c 344 g 201 t 11 others
ORIGIN

Query Match

Best Local Similarity 97.7%; Pred. No. 3.1e-141;
Matches 882; Conservative 9; Mismatches 10; Indels 2; Gaps 2;

420 GCTTATATGGGGTCAACAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 478

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Db 1009 GCTTATGGGGTCAACAGACCCGCCGCCGCCGCCGCCGCCCAATTCTCTCC 950
OY 479 AGCTCAACTGCAAAAGCTCTTTCTTCAGACATGAGATCACGAGCTGGAGTTGTT 538
Db 949 AGCTCAACTGCAAAAGCTCTTTCTTCAGACATGAGATCACGAGCTGGAGTTGTT 890
OY 539 CAGATCATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 598
Db 889 CAGATCATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 830
OY 559 AGCCACTTCAAGCTCTGCAAGGCTCTGCAAGGCTCTGCAAGGCTCTGCAAGGCTCTG 658
Db 829 AGCCACTTCAAGCTCTGCAAGGCTCTGCAAGGCTCTGCAAGGCTCTGCAAGGCTCTG 770
OY 659 GAAGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 718
Db 769 GAAGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 710
OY 719 GAATCCCAAGAGCCGAGGCTTACGCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCG 778
Db 709 GAATCCCAAGAGCCGAGGCTTACGCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCG 651
OY 779 CCCTTCGCGCCAGGCGGAGGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCT 838
Db 650 CCCTTCGCGCCAGGCGGAGGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCT 591
OY 839 GAGATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 898
Db 590 GAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 531
OY 899 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 958
Db 530 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 471
OY 959 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1018
Db 470 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 411
OY 1019 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1078
Db 410 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 351
OY 1079 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1138
Db 350 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 291
OY 1139 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1198
Db 290 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 231
OY 1199 CACACACACATGCGCGCTTACAGAGCGAGCGATCTGAGCAAGAGAGATTAACAG 1258
Db 230 MACACACACATGCGCGCTTACAGAGCGAGCGATCTGAGCAAGAGAGATTAACAG 171
OY 1259 AAAGACACCTCTCTTACAGGCTCCCAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1318
Db 170 AAAGACACCTCTCTTACAGGCTCCCAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 111
OY 1319 CAG 1321
Db 110 CAG 108

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RESULT 3
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DEFINITION AGENCOURT_8287174 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:6292265
5', mRNA sequence.
ACCESSION B0641849
VERSION B0641849.1 GI:21766021
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homini; Homo.
1 (bases 1 to 967)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LILN at:
http://image.llnl.gov
Plate: LILN2493 row: g column: 18
High quality sequence stop: 571.
Location/Qualifiers
1. 967
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/notes="Organ: eye; Vector: pORF1; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library. !"
BASE COUNT
194 a 334 c 296 g 143 t
ORIGIN
Query Match 58.0%; Score 766.8; DB 13; Length 967;
Best Local Similarity 99.1%; Pred. No. 5.5e-125;
Matches 771; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 524 GAGCTGAGTTGTTGATCATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 583
Db 1 GAGCTGAGTTGTTGATCATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
OY 584 ATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 643
Db 61 ATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
OY 644 CAGGGGCGAGAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 703
Db 121 CAGGGGCGAGAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
OY 704 ACAGTGTACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 763
Db 181 ACAGTGTACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 240
OY 764 GAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 823
Db 241 GAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
OY 824 CCGTACCTGACAGAGATGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 883
Db 301 CCGTACCTGACAGAGATGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 360
OY 884 CCCCACCTTACAGAGGCGCGCTGACCTTCAAGCTTGGGAGCCCGAGAGAGAGAGAGAG 943
Db 361 CCCCACCTTACAGAGGCGCGCTGACCTTCAAGCTTGGGAGCCCGAGAGAGAGAGAGAG 420
OY 944 CTGAACCGGAGTGGTGGCGCGAGCCCGCAACCAAGCAACATCTTGACAGTACCTGAG 1003
Db 421 CTGAACCGGAGTGGTGGCGCGAGCCCGCAACCAAGCAACATCTTGACAGTACCTGAG 480

```

OY 1004 GATATGCCAGGCTGGGGGCCCCCCCCCAGACAGTAACTCGGGCATGAGCCACG 1063
 DB 481 GATATGCCAGGCTGGGGGCCCCCCCCCAGACAGTAACTCGGGCATGAGCCACG 540
 OY 1064 TGCTACGGCAGGGGGGGGCGGATGAGGGGGCGCCGCCACTTACAGGAGGTCTATCGGC 1123
 DB 541 TGCTACGGCAGGGGGGGGCGGATGAGGGGGCGCCGCCACTTACAGGAGGTCTATCGGC 600
 OY 1124 CACTACCGGGGTCCTCTCTCCAGACACGACAGAGCAGTGGGGCCCTCTTGGTGGAG 1183
 DB 601 CACTACCGGGGTCCTCTCTCCAGACACGACAGAGCAGTGGGGCCCTCTTGGTGGAG 660
 OY 1184 GGGGACCGGGTCACACACACACATCGCCGCCCTTACAGAGCGACCATTTGAGCAAA 1243
 DB 661 GGGGACCGGGTCACACACACATCGCCGCCCTTACAGAGCGACCATTTGAGCAAA 720
 OY 1244 GAGAGAGTAAACAGAAAGACACCTCTTAGGGTCCCGAGGGGGGGGGGCTGGG 1301
 DB 721 GAGAGAGTAAACAGAAAGACACCTCTTAGGGTCCCGAGGGGGGGGGGCTGGG 778

RESULT 4
 BM922276 1046 bp mRNA linear EST 12-MAR-2002
 LOCUS AGENCOURT.6707077 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5754437
 ACCESSION BM922276
 VERSION BM922276.1 GI:19372655
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 1046)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: gcrabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LLNL2791 row: n column: 06
 High quality sequence stop: 671.
 Location/Qualifiers
 1. 1046

FEATURES
 source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5754437"
 /lab_host="DH10B"
 /clone_id="NIH_MGC_115"
 /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research genetics tracking code 021. Note: this is a NIH_MGC Library."
 BASE COUNT 205 a 391 c 298 g 150 t 2 others
 ORIGIN

Query Match 58.0%; Score 766; DB 12; Length 1046;
 Best Local Similarity 95.8%; Pred. No. 7.6e-125;
 Matches 818; Conservative .0; Mismatches 32; Indels 4; Gaps 3;

OY 347 CCGGCGGAGGCCCCCCCCCGGGCCCCGAGCCCCCCCCCGGGCCCCGGCCGCCG 406
 DB 1 CCGGCGGAGGCCCCCCCCCGGGCCCCGAGCCCCCCCCCGGGCCCCGGCCGCCG 60
 OY 407 CCGTCATATGACCCGCTTATGATGGGGGTCAACAGCACCCGCGCGCGCGGAGACCC 466
 DB 61 CCGTCATATGACCCGCTTATGATGGGGGTCAACAGCACCCGCGCGCGCGGAGACCC 120
 OY 467 AATCTCTCTGACAGTGTGCACTGTCAAAAGCTCTTTGTTCCAGAGATGAGATCAGAG 526
 DB 121 AATCTCTCTGACAGTGTGCACTGTCAAAAGCTCTTTGTTCCAGAGATGAGATCAGAG 180
 OY 527 CTGAGATTGTTGATGATCATATCATGTGTGTGTGTATGATGGATGGATGGTGGATC 586
 DB 181 CTGAGATTGTTGATGATCATATCATGTGTGTGTGTATGATGGATGGTGGATC 240
 OY 587 ACGTGCCTGTGAGCCACTACAAAGCTGTGCAAGGTCTTTCATACAGCCGACAGCAG 646
 DB 241 ACGTGCCTGTGAGCCACTACAAAGCTGTGCAAGGTCTTTCATACAGCCGACAGCAG 300
 OY 647 GGGGGSAGAGAGAAATGCGCTGTCTCTCAGAAAGATGCTGTGGCCCTTGAGAGCACA 706
 DB 301 GGGGGSAGAGAGAAATGCGCTGTCTCTCAGAAAGATGCTGTGGCCCTTGAGAGACACA 360
 OY 707 GTGTCAAGCAAGCAATCCAGAGCCGACAGGTCTACGCCCGCGCTGGGCCACGACCGG 766
 DB 361 GTGTCAAGCAAGCAATCCAGAGCCGACAGGTCTACGCCCGCGCTGGGCCACGACCGG 420
 OY 767 CTGGCGGTGCGCGCTTCCGCCACAGGGGAGCGCTTCCACGCTTCCAGCCACCTATCCG 826
 DB 421 CTGGCGGTGCGCGCTTCCGCCACAGGGGAGCGCTTCCACGCTTCCAGCCACCTATCCG 480
 OY 827 TACCTGACAGCAGATGACGACGTCGACCCACCATCTCGGTGACAGGGGAGAGGCC 886
 DB 481 TACCTGACAGCAGATGACGACGTCGACCCACCATCTCGGTGACAGGGGAGAGGCC 540
 OY 887 CAACCTTACAGAGGCGCCCTGACACCTTCAGAGTTCGGAGCCCGACAGCAGTGTGAATCG 946
 DB 541 CAACCTTACAGAGGCGCCCTGACACCTTCAGAGTTCGGAGCCCGACAGCAGTGTGAATCG 600
 OY 947 AACCGGAGATGCGGTGGGCGACCCCAACACAGAACCATCTTGGACAGTACCTGATGAT 1006
 DB 601 AACCGGAGATGCGGTGGGCGACCCCAACACAGAACCATCTTGGACAGTACCTGATGAT 660
 OY 1007 AGTGCCAGGTGGGCGCCCTGCGCCCGCCAGAGATTAATCGGGCATCGAGCGATCG 1066
 DB 661 AGTGCCAGGTGGGCGGCGCCCTGCGCCCGCCAGAGATTAATCGGGCATCGAGCGATCG 720
 OY 1067 TACGCGACGCGCGG-CCGATGAGAGGGGCGCGCG-CCACCTTACAGCGAGTCAATCGGCG 1124
 DB 721 TACGCGACGCGCGGCGCCGATGAGAGGGGCGCGCGCCGCTTACAGAGGAGTCAATCGGCG 780
 OY 1125 ACTA--CCCGGGGTCTCTCTCCAGACACGACAGAGCAGTGGGCCCTCTTCTGGA 1182
 DB 781 ACTAAGCGGGGCTCTCTCTCCAGACACGACAGTGGGCCCTCTCTGGA 840
 OY 1183 GGGGACCGCGCTC 1196
 DB 841 CTGGAAGGGGAAC 854

RESULT 5
 AL543170 1201 bp mRNA linear EST 31-MAY-2003
 LOCUS AL543170 Homo sapiens PLACENTA cot 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS0D1002Y103 5-PRIME, mRNA sequence.
 ACCESSION AL543170
 VERSION AL543170.2 GI:31265017
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

Query Match	55.7%;	Score 736.4;	DB 13;	Length 916;
Best Local Similarity	95.7%;	Pred. No. 1.2e-119;		
Matches 800; Conservative	0;	Mismatches 31;	Indels 5.	Cane 4

[illegible]

RESULT 7	AL558881/c	LOCUS	DEFINITION	ACCESSION
	AL558881	951 bp	MRNA	linear
	AL558881	Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED		
	Homo sapiens cDNA clone CSDDJ015YF12 3-PRIME, MRNA sequence.			
	AL558881			

VERSION	AL558881.2	GI:31283014
KEYWORDS	EST.	
SOURCE	Homo sapiens	(human)
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Euteleia; Primates; Catarrhini; Homnidae; Homo.	
TITLE	1 (bases 1 to 951)	
JOURNAL	Li, W.B., Gruber, C., Jassee, J. and Polayes, D.	
COMMENT	Full-length cDNA libraries and normalization	
	Unpublished	
	On Feb 15, 2001 this sequence version replaced GI:12902826	

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FEATURES
source      Location/Qualifiers
1. .951     . : CCGGDDGDDGCGC008NP1.

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BASE COUNT	141 a	275 c	318 g	201 t	16 others
ORIGIN					

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Query Match      55.68; Score 735; DB 9; Length 951;
Best Local Similarity 99.1%; Pred. No. 2.1e-119;
Matches 738; Conservative 1; Mismatches 6; Indels 0; Gaps 0
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QY	577	GATGGTATGACAGGCGCGCTGCGTGGACCACTACAAAGCTGTCTGACAGCGTCTTCATCAACCG	636
Db	854	GGATGTGTTACACGTGCGCTGCGTGGACCACTACAAAGGTGTCTGACAGCGTCTTCATCAACCG	795
QY	637	GCACAGCCAGAGGGGCGAGAGAGAAAGTACCCTGTCTCTCAGAAAGATGCGTGGCCCTC	836
Db	794	GAACAGCCAGAGGGGCGAGAGAAAGTACCCTGTCTCTCAGAAAGATGCGTGGCCCTC	735
QY	697	GGAGAGCAACAGTTCAGAGCAAGGAATCCAGAGCCGAGGTCACGCCCGCGCTGAGGC	756
Db	734	GGAGAGCAACAGTTCAGAGCAAGGAATCCAGAGCCGAGGTCACGCCCGCGCTGAGGC	675
QY	757	CACGAGACCGCTGTGGCGGTGCGCGCCCTTGCGCCAGGGAGGGCGCTTCACCGCTTCCAGCC	816
Db	674	CACGAGACCGCTGTGGCGGTGCGCGCCCTTGCGCCAGGGAGGGCGCTTCCACCGCTTCCAGCC	615
QY	817	CACCTTCCGTTACTCTGACAGCACGAGATGACCTGCCAACCCAGCATCTCGCTGCAGACGG	876
Db	614	CACCTTCCGTTACTCTGACAGCACGAGATGACCTGCCAACCCAGCATCTCGCTGCAGACGG	555
QY	877	GGAGAGAGCCCCACACCTTACACAGGGGCGCGTGCACCTTCACACTTTCGGGACCCGAGCAGCA	936
Db	554	GGAGAGAGCCCCACACCTTACACAGGGGCGCGTGCACCTTCACACTTTCGGGACCCGAGAGCA	495
QY	937	GCTGGAACTGAAACCGGGAGTGGGTGGCGCACCCCAAGAGAACCATCTTGACAGCAGGA	996
Db	494	GCTGGAACTGAAACCGGGAGTGGGTGGCGCACCCCAAGAGAACCATCTTGCAGACAGGA	435
QY	997	CTGTAGTGAATGTGCAAGCTGGGGCGCCCTGTGCCCGCCACGACGATTACTCGGGGATATG	1056

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Db 434 CCTGATGGATGCTGAGGCTGGGGCCCTGCCCCCCACAGCACTGCGGATCG 375
OY 1057 CCGCAGCTGTACGGCAGCGGGCGCATGAGGGGGCGCGCCACCTACAGCAGGT 1116
Db 374 CGCCAGCTGTACGGCAGCGGGCGCATGAGGGGGCGCGCCACCTACAGCAGGT 315
OY 1117 CATGGCCACTACCCGGGGCTCTCTTCCAGCAGCAGCAGAGTGGGGCGCCCTCTT 1176
Db 314 CATCGCCACTACCCGGGGCTCTCTTCCAGCAGCAGCAGAGTGGGGCGCCCTCTT 255
OY 1177 GGTGAGGGAGCCGGGCTCCACACACACATCGCGCCCTAGAGAGGGCAGCATCTG 1236
Db 254 GGTGAGGGAGCCGGGCTCCACACACATCGCGCCCTAGAGAGGGCAGCATCTG 195
OY 1237 GAGCAAGAAGAGATTAACAAGAAAGACACCCCTCTTAGGGTCCCGAGGGGGCGGAC 1296
Db 194 GAGCAAGAAGAGATTAACAAGAAAGACACCCCTCTTAGGGTCCCGAGGGGGCGGAC 135
OY 1297 TGGGGCTGCTAGTGTGAAAAAGGACG 1321
Db 134 TGGGGCTGCTAGTGTGAAAAAGGACG 110

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RESULT 8
LOCUS AL558882 1007 bp mRNA linear EST 31-MAY-2003
DEFINITION AL558882 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
ACCESSION AL558882 Homo sapiens cDNA clone CS0DJ015YF12 5-PRIME, mRNA sequence.
VERSION AL558882.2 GI:31283015
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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REFERENCE 1 (bases 1 to 1007)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 15, 2001 this sequence version replaced gi:12903838.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
9945.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DJ015DC06P1&cluster=9945.r. Contact :
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0DJ015DC06P1.

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FEATURES
Source
Location/Qualifiers
1..1007
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ015YF12"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/clone_line="JURKAT"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

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BASE COUNT 218 a 325 c 292 g 151 t
ORIGIN

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Query Match 54.2% Score 715.4 DB 9: Length 1007;
Best Local Similarity 99.1% Pred. No. 5.8e-116;
Matches 738: Conservative 2; Mismatches 3; Indels 2; Gaps 2;

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OY 577 GGTGTGATCAGTGTGCTCTGAGCCATCAAGCTGTGTGACGGTCCCTTATCAGCCG 636
Db 62 GGATGTGATCAGTGTGCTCTGAGCCATCAAGCTGTGTGACGGTCCCTTATCAGCCG 121
OY 637 GCACAGCCAGGGGGGAGAGAGAGATCCCTGTCTCAGAGAGATGCTGTGGCCCTC 696
Db 122 GCACAGCCAGGGGGGAGAGAGAGATCCCTGTCTCAGAGAGATGCTGTGGCCCTC 181
OY 697 GGAGAGCAGATGTACAGGAGAGAGATCCCAAGCCGAGTCTAGCCCGCCCTTCGGCC 756
Db 182 GGAGAGCAGATGTACAGGAGAGAGATCCCAAGCCGAGTCTAGCCCGCCCTTCGGCC 240
OY 757 CACGAGCCCTGTGGCCCTGCGCCCTTCCAGAGGGAGAGCCCTTCCAGCCAGCC 816
Db 241 CACGAGCCCTGTGGCCCTGCGCCCTTCCAGAGGGAGAGCCCTTCCAGCCAGCC 300
OY 817 CACCTATCCGTACTGACAGCAGAGATGACCTGCCACCCATCTGCTGTACAGAGC 876
Db 301 CACCTATCCGTACTGACAGCAGAGATGACCTGCCACCCATCTGCTGTACAGAGC 360
OY 877 GGAGAGCCCGCCACCTACAGGGCCCGCCGACCCCTCCAGTCTGGGAGCCCGAGAGCA 936
Db 361 GGAGAGCCCGCCACCTACAGGGCCCGCCGACCCCTCCAGTCTGGGAGCCCGAGAGCA 420
OY 937 GCTGGAAGTGAACCGGAGTGGTGGCGCGCACCCCAACAGAACATCTTGCAGAGTGA 996
Db 421 GCTGGAAGTGAACCGGAGTGGTGGCGCGCACCCCAACAGAACATCTTGCAGAGTGA 480
OY 997 CCTGATGATAGTGTCCAGAGCTGGGGCCCTGCCCCCAGCAGTAACTGTGGGATCAG 1056
Db 481 CCTGATGATAGTGTCCAGAGCTGGGGCCCTGCCCCCAGCAGTAACTGTGGGATCAG 540
OY 1057 CGCCAGCTGTACGGGAGGGGGGGGAGTGAAGGGGGCGCCGCCACCTACAGCAGGT 1116
Db 541 CGCCAGCTGTACGGGAGGGGGGGGAGTGAAGGGGGCGCCGCCACCTACAGCAGGT 600
OY 1117 CATGGCCACTACCCGGGGCTCTCTTCCAGCAGCAGCAGAGTGGGGCGCCCTCTT 1176
Db 601 CATGGCCACTACCCGGGGCTCTCTTCCAGCAGCAGCAGAGTGGGGCGCCCTCTT 660
OY 1177 GGTGAGGGGAGCCGGGCTCCACACACATCGCGCCCTAGAGAGGGCAGCATCTG 1236
Db 661 GGTGAGGGGAGCCGGGCTCCACACACATCGCGCCCTAGAGAGGGCAGCATCTG 719
OY 1237 GAGCAAGAAGAGATTAACAAGAAAGACACCCCTCTTAGGGTCCCGAGGGGGCGGAC 1296
Db 720 GAGCAAGAAGAGATTAACAAGAAAGACACCCCTCTTAGGGTCCCGAGGGGGCGGAC 779
OY 1297 TGGGGCTGCTAGTGTGAAAAAGGACG 1321
Db 780 TGGGGCTGCTAGTGTGAAAAAGGACG 804

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RESULT 9
LOCUS BX362396/c 874 bp mRNA linear EST 05-MAY-2003
DEFINITION BX362396 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
ACCESSION BX362396 Homo sapiens cDNA clone CS0DJ014YNI 3-PRIME, mRNA sequence.
VERSION BX362396.1 GI:30378625
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 874)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France

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OY 679 AGGATGCTGTGGCCCTGGAGAGCAGTGTCTAGGCAAGGAAATCCAGAGCCGAGT 738
DB 245 AGGATGCTGTGGCCCTGGAGAGCAGTGTCTAGGCAAGGAAATCCAGAGCCGAGT 304
OY 739 CTACGCCCCGCTCGGCCACCGAGCCGCTGGCCGCTTGGCCCTGAGGAGG 798
DB 305 CTACGCCCCGCTCGGCCACCGAGCCGCTGGCCGCTTGGCCCTGAGGAGG 364
OY 799 CTTCCACCGCTTCAGAGCCACCTATCTGCTAGCAGCAGAGATGACCTCCACCCAC 858
DB 365 CTTCCACCGCTTCAGAGCCACCTATCTGCTAGCAGCAGAGATGACCTCCGCGCCAC 424
OY 859 CATCTCGCTGTAGAGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 918
DB 425 CATCTCGCTGTAGAGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 484
OY 919 TCGGAGCCCCGAGCAGAGCTGGAAGTGAAGCGGAGAGTGGTGGCGGAGCCGCAAAACAG 978
DB 485 TCGGAGCCCCGAGCAGAGCTGGAAGTGAAGCGGAGAGTGGTGGCGGAGCCGCAAAACAG 544
OY 979 AACCATCTTCGACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1038
DB 545 AACCATCTTCGACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 604
OY 1039 CAGTAACTCGGGGATCAGAGCGCCAGCTGCTACGAGCAGAGCGGCGGCGATGAGAGCGCGC 1098
DB 605 CAGTAACTCGGGGATCAGAGCGCCAGCTGCTACGAGCAGAGCGGCGGCGATGAGAGCGCGC 664
OY 1099 GCCCAGCTACAGAGAGTGTATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1158
DB 665 GCCCAGCTACAGAGAGTGTATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 724
OY 1159 CAGTGGGCGGCGCTTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1216
DB 725 CAGTGGGCGGCGCTTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 784
OY 1217 CTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1271
DB 785 CTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 844
OY 1272 TCTAAGGCTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1306
DB 845 TTCTAGGCTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 879

RESULT 11
BU602918 850 bp mRNA linear EST 20-SEP-2002
LOCUS REF10016502 NIH_MGC_142 Homo sapiens cDNA clone
DEFINITION IMAGE:6497853 5', mRNA sequence.
ACCESSION BU602918
VERSION BU602918.1 GI:23254677
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 850)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: NCI
cDNA Library Preparation: Michael Brownstein Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Cloning distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2679 row: 1 column: 22
High quality sequence stop: 499.
Location/Qualifiers

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source
1. 850
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6497853"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (71-phage-resistant)"
/clone_11b="NIH_MGC_142"
/Note="Vector: pDNR-LIB; Site 1: SfiI (ggccattagc);
Site 2: SfiI (ggcgctcgccg); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
2%, blood - 33.4%, brain - 5.6%, breast - 12.3%, colon
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,
ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary
gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were
used in cloning as follows:
5'-AAGCACTGCTATCAAGCAGATGAGTGGCCATTAGCCGCGG-3' and
5'-ATTCTAGAGCCGAGGCGGCGCCGACATG-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the >0.5 kb
size fraction (other fractions present in NIH_MGC_141).
Library created in the laboratory of M. Brownstein (NIH,
NIH). Note: this is a NIH_MGC Library."
BASE COUNT 173 a 303 c 251 g 123 t
ORIGIN
Query Match 52.0%; Score 686.6; DB 13; Length 850;
Best Local Similarity 96.9%; Pred. No. 6.6e-111;
Matches 743; Conservative 0; Mismatches 19; Indels 5; Gaps 4;
OY 559 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 618
DB 1 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60
OY 619 AGGATCTTCATCAGCCGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 678
DB 61 AGGATCTTCATCAGCCGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
OY 679 AGGATGCTGTGGGCGCTTGGAGAGCAGAGTGTGAGCAAGAGAGAGAGAGAGAGAGAGT 738
DB 121 AGGATGCTGTGGGCGCTTGGAGAGCAGAGTGTGAGCAAGAGAGAGAGAGAGAGAGAGT 180
OY 739 CTACGCCCCGCTCGGCCACCGAGCCGCTGGCCGCTTGGCCCTGAGGAGGAGG 798
DB 181 CTACGCCCCGCTCGGCCACCGAGCCGCTGGCCGCTTGGCCCTGAGGAGGAGGAGG 240
OY 799 CTTCCACCGCTTCAGAGCCACCTATCTGCTAGCAGCAGAGATGACCTCCACCCAC 858
DB 241 CTTCCACCGCTTCAGAGCCACCTATCTGCTAGCAGCAGAGATGACCTCCACCCAC 300
OY 859 CATCTCGCTGTAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 918
DB 301 CATCTCGCTGTAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 360
OY 919 TCGGAGCCCCGAGCAGAGCTGGAAGTGAAGCGGAGAGTGGTGGCGGAGCCGCAAAACAG 978
DB 361 TCGGAGCCCCGAGCAGAGCTGGAAGTGAAGCGGAGAGTGGTGGCGGAGCCGCAAAACAG 420
OY 979 AACCATCTTCGACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1038
DB 421 AACCATCTTCGACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 480
OY 1039 CAGTAACTCGGGGATCAGAGCGCCAGCTGCTACGAGCAGAGCGGCGGCGATGAGAGCGCGC 1098
DB 481 CAGTAACTCGGGGATCAGAGCGCCAGCTGCTACGAGCAGAGCGGCGGCGATGAGAGCGCGC 540
OY 1099 GCCCAGCTACAGAGAGTGTATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1158
DB 541 GCCCAGCTACAGAGAGTGTATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
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Db	601	CAGTGGGCGGCCCTCTTGCTGGAAAGGGAGACCCGGCTTCACACACACAACAATCCGGCC	660
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Db	661	CTTAAGAGCAGCAGCATTTCTGAGACAACAAATGATTAACCGAAGAAGCACCCCTCTCTA	720
Oy	1276	GGGTCCCCAGGGGGGC--GGGCTGTGGGCTCGTAGTGAAGAAAGCA	1320
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AKO08976			
LOCUS			
DEFINITION			
Accession			
Version			
Keywords			
Source			
Organism			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
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PUBMED	11217851
REFERENCE	5
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 1207)
AUTHORS	Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furukoshi,Y., Furuhara,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hisaoke,T., Horii,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,I., Kojima,Y., Komori,H., Kouda,M., Koya,S., Kuribara,C., Matsuyama,T., Miyazaki,A., Nishik,K., Nomura,K., Numasaki,R., Ohno,M., Okazaki,Y., Ohtdo,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibusaki,M., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toyota,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUN-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsr.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	Please visit our web site (http://genome.gsc.riken.go.jp/) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAAGACGCCAGACTCTTTTTCCTTTTTTTTAA 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGTCCGTAATTAAATTAATCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOLR.
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Query Match	47.7%; Score 630.6; DB 11; Length 1207;


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LOCUS      782 bp mRNA linear EST 26-MAR-2002
DEFINITION U1-H-ED1-axx-k-20-0-U1.s1 NCI_CGAP_ED1 Homo sapiens cDNA clone
IMAGE:5834635 3', mRNA sequence.
VERSION    BQ015170.1 GI:19740071
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 782)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL    Unpublished
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgaps-femail.nih.gov
           Tissue Procurement: Dr. Jose Mercuende
           cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
           DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
           Clone Distribution: Clone distribution information can be found
           through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
           Seq primer: M13 FORWARD
           POLYA-yes.
FEATURES   location/Qualifiers
SOURCE     1..782

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Site:2: Not I; NCI_CGAP_ED1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line C55. The library was constructed according to Bonaldo
, Lennon and Soares, Genome Research, 6:791-806, 1996.
First strand cDNA synthesis was primed with an oligo-dT
primer containing a Not I site. Double stranded cDNA was
ligated to an EcoR I adaptor, digested with Not I, and
cloned directionally into pT73-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCTCAAGGCT.
TAG_LIB-U1-H-ED1
TAG_TISSUE=chondrosarcoma
TAG_SEQ=CGTCAAGCT"

BASE COUNT      109 a      223 c      176 t      3 others
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Best Local Similarity 98.9%; Pred. No. 2,9e-98;
Matches 617; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db      782 GAGAGCAGTGTGACGAGCAAGATCCAGAGCCGAGGTACGCCCGCTCGGCC 723
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Db      722 ACCGAGCGCTGGCGCTGGCGCTTGGCCGAGCGGAGCGGTCCACCGCTTCAGGCC 663
QY      818 ACCTATCGCTACTGTGAGCAGAGATGACCTGACCCACCATCTCGCTGTCAGAGCG 877
Db      662 ACCTATCGCTACTGTGAGCAGAGATGACCTGACCCACCATCTCGCTGTCAGAGCG 603
QY      878 GAGAGCCCCCACCCTTACAGAGGGGCCCTGACCTTGGGAGCCCGAGAGCAG 937
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Db      542 CTGGAAGTGAACGGGAGTGGGTGGCGGACCCCAAGAGAACATCTTCAAGTGC 483
QY      998 CTGATGATAGTGCAGAGGTGGGCGCCCTGCCCCCAGCAGTAACTCGGGCATCAG 1057
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QY      1058 GCCAGTGTCTACGGCAGCGGGCGCGATGAGAGGGCCCGCCACCTACAGCGAGG 1117
Db      422 GCCAGTGTCTACGGCAGCGGGCGCGATGAGAGGGCCCGCCACCTACAGCGAGG 363
QY      1118 ATGGCGCCTACCCGGGGGTCTCTCTTCCAGCAGCAGAGCAGTGGGCGCTCTCTG 1177
Db      362 ATGGCGCCTACCCGGGGGTCTCTCTTCCAGCAGCAGAGCAGTGGGCGCTCTCTG 303
QY      1178 CTGAGAGGGAGCCCGGCTCCACACACACATCGCGCCCTTACAGAGCGAGCATGTG 1237
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QY      1298 GGGGCTGCTGATGATGAAGAGCAG 1321

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      DEFINITION  hd13h06.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he
      ACCESSION   B0636742
      VERSION     B0636742.1 GI:21761201
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      SOURCE      Homo sapiens (human)
      ORGANISM    Homo sapiens
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
      Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behl,A., Touchman
      J.W., Bouffard,G., Smith,D. and Peterson,K.
      Expressed sequence tag analysis of human retina for the NEIRBank
      Project: Retbindin, an abundant, novel retinal cDNA and alternative
      splicing of other retina-preferred gene transcripts
      Mol. Vis. 8 (4), (2002) in press
      Contact: Wistow G
      Section on Molecular Structure and Function
      National Eye Institute
      6/331, NIH, Bethesda, MD 20892-2740, USA
      Tel: 301 402 3452
      Fax: 301 496 0078
      Email: graeme@helix.nih.gov
      Plate: 13 row: h column: 06
      Seq primer: M13RP1 reverse primer (ABI).
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          /note="Organ: Eye; Vector: pSPORT1; Neural retina tissue
          was dissected from two 80 year old donors with no observed
          eye disease. 100ug of total RNA was used for library
          construction. A directionally cloned cDNA library in the
          pSPORT1 vector (Life Technologies) was constructed at
          Bioserve Biotechnology (Laurel MD) essentially following
          the protocols of the SuperScript Plasmid System full
          details of which are contained in the manufacturer's
          instruction manual (http://www.lifetech.com/). First
          strand synthesis was carried out using a Not I
          primer-adaptor [5'-pGACTAGTCTAATCCGAGCGCCGCC(TT)15-3'
          ]. EST analysis was performed on the unamplified library
          at the NIH Intramural Sequencing Center (NISC)."
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BASE COUNT 114 a 238 c 182 g 75 t

ORIGIN

Query Match 46.0%; Score 607.4; DB 13; Length 609;
 Best Local Similarity 99.8%; Pred. No. 5.2e-97;
 Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 691 GCCCTGGAGAGACAGTGTACGCAACGGAATCCAGAGCCGACAGTCTACGCCGCC 750
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OY 751 TGGGCCACCGACCGCTGCGCCCTTGCCTCCAGCGGAGCGCTCCACCGCTT 810
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Db 121 TGGGCCACCGACCGCTGCGCCCTTGCCTCCAGCGGAGCGCTCCACCGCTT 180
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OY 871 AGACGGGAGAGAGACCCCAACCCCTACCAAGGCCCCCTGACCCCTTCAGCTTCGGAGCCGCA 930
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Search completed: August 27, 2003, 20:08:54
 Job time : 3118 secs

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; Sequence 2, Application US/09769482			
; Patent No. 6566130			
; GENERAL INFORMATION:			
APPLICANT: SRIYASTAVA, SHIV			
APPLICANT: MOUL, JUDD W.			
APPLICANT: XU, LINDA L.			
TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED			
TITLE OF INVENTION: POUXNUCLEOTIDE ARRAY			
FILE REFERENCE: 04995-0057-00000			
CURRENT APPLICATION NUMBER: US/09/769,482			
PRIOR APPLICATION NUMBER: 2001-01-26			
PRIOR FILING DATE: 2000-01-28			
PRIOR APPLICATION NUMBER: 60/179,045			
PRIOR FILING DATE: 2000-01-31			
NUMBER OF SEQ ID NOS: 67			
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SEQ ID NO 2			
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US-09-769-482-2			

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Best Local Similarity	99.7%	755.8	4	755
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Db	661	CTGAGAGGGGACCCGGCTCTCCACACACACATCTGGGCGCCCTAGAGAGCGCAGCCATCTGG	720
OY	1238	AGCAAGAGAGAGATTAACAGAAAGACACCTCTCTAG	1276
Db	721	AGCAAGAGAGAGATTAACAGAAAGACACCTCTCTAG	759

RESULT 3
 US-09-091-952A-7
 : Sequence 7, Application US/09091952A
 : Patent No. 6458532
 : GENERAL INFORMATION:
 APPLICANT: Detera-Wagleigh, Sevilla D.
 Gershon, Elliot S.
 Badner, Judith A.
 Goldin, Lynn R.
 Berrettini, Wade H.
 Yoshikawa, Takeo
 Sanders, Alan R.
 Esterling, Lisa E.
 TITLE OF INVENTION: Chromosomal Markers and Diagnostic
 Tests for Manic-Depressive Illness
 NUMBER OF SEQUENCES: 197
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94111-3834

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 1...921
OTHER INFORMATION: Clone 22 coding region
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-091-952A-7

Query Match      26.7%: Score 352.2: DB 4: Length 921:
Best Local Similarity 73.1%: Pred. No. 9.5e-58:
Matches 482: Conservative 0: Mismatches 168: Indels 9: Gaps 2

QY 506 CAGACATGAGAGATCAGCAGAGCTGGAGTTTTCAGATCATCATCATCGTGGTGTGATG 565
Db 166 CCGGGCATCTTCAACTCGGAGCTGGAGTTCGCCCAATCATCATCATCGTGGTGTG 225
QY 566 ATGTGTATGTGTGTGTGTATCAGCTGCCCTGCTGAACCACTACAAGCTGTGTGACGTTCC 625
Db 226 ACGGTGATGTGTGTGTGTATCAGCTGCCCTGCTGAACCACTACAAGCTGTGTGACGTTCC 285
QY 626 TTCAATCAGCCCGGACACAGCAGGCGCGGAGAGAGAAAGATGCCCTGTCTCTCAGAAAGATGC 685
Db 286 TTCTATCAACCCCGGACACAGGCGCGGAGAGAGAGAGATGCCCTGTCTCTCAGAAAGATGC 345
QY 686 CTGTAGCCCTTGGAGAGACAGATGTCAAGGAAAGGATCCAGAGCCGACAGGTCTAAGCC 745
Db 346 CTGTAGCCCTTGGAGAGACAGGCGCGGACAGGCGGCTGGG-----CGCTCGGAATCATGAT 399
QY 746 CGGCTCGGGCCACCGACGCGCTGGCGCTGCCTTCGCCACAGGAGAGCGCTTCCAC 805
Db 400 GCGCCGCGGCTCAAGGAGACAGGTTCAACAGCGCGCTTCCTTCAACAGAGGATCGCTTACG 459
QY 806 CGCTTCCAGCCCACTATTCGTACCTGACAGACAGATGACATGTGCCACCAACCATATCTCG 865
Db 460 CGCTTCCAGCCCACTATTCGTACCTGACAGACAGATGATGATCTTCTCCACCATCTCC 519
QY 866 CTGTACAGCGGGAGAGAGCCCGACACCCATACAGAGGCGCTGACCTGACCTGACGTTGGAG 925
Db 520 CTGTTCAGCGGTGAAGAGCCACCTCTTACAGAGGCGCTGACCTGACCTGACGTTCCGGAG 579
QY 926 CCGGAGCAGCAGCTGGAATAGTAAGACGAGAGTGTGTGCGCGAGACCCCAAGAAAGAACATC 985
Db 580 CCTGAGCAGCAGATGGAATCAACCGAAGTGTGTGTGAGGCGCCCAACCAAGAACATCA 639
QY 986 TTCGACAGTACCTGATGATGATGTGCCAGG---CTGGGCGGGCGCCCTGCCCCCAAGCAAGT 1042

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Db 640 TTTCAGCATGATTTTAATGACATTTCCTATGTAATAGCCGGGGGTCATTGCCACCCAGCAGC 699

Qy 1043 AACTCGGCGCATCAGCCGCCACGCTGCTACGACGAGCGCGCCGCATGAGAGGGCCGCCGCC 1102

Db 700 AACTCGGCGCATCAGTGCAGACGCTGCAGCAGAGTAAACGGAGAGATGAGAGGGCCACGCCCC 759

Qy 1103 ACCTACGACGCGGCTCATCGCCCACTACCCGGGGCTCTCTTCACGACACGACGAGCAG 1161

Db 760 ACATACGACGAGGTGATGGCGCACCCAGCCGCGCTCTTCTTCATCACCAGCGCAG 818

RESULT 4

US-09-091-952A-6

Sequence 6, Application US/09091952A

Patent No. 6458532

GENERAL INFORMATION:

APPLICANT: Detera-Madleigh, Sevilla D.

Gershon, Elliot S.

Badner, Judith A.

Goldin, Lynn R.

Berretini, Wade H.

Yoshikawa, Takeo

Sanders, Alan R.

Berterling, Lisa E.

TITLE OF INVENTION: Chromosomal Markers and Diagnostic Tests for Manic-Depressive Illness

NUMBER OF SEQUENCES: 197

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/091,952A

FILING DATE: 19-Apr-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/029,278

FILING DATE: 28-OCT-1996

APPLICATION NUMBER: PCT/US97/19381

FILING DATE: 28-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Smith, Timothy L.

REGISTRATION NUMBER: 35,367

REFERENCE/DOCKET NUMBER: 015280-297100US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 8065 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: -

LOCATION: 1...8065

OTHER INFORMATION: Clone 22

FEATURE:

NAME/KEY: CDS

LOCATION: 116...1036

OTHER INFORMATION: Clone 22 coding region

FEATURE:

QY	CTGTCAAGCGGGGAGAGACCCCCCAACCCATACAGGGGCCCTGTACACCTTCACCTTCGGGAC	925
QY <td>866 CTGTCAAGCGGGGAGAGACCCCCCAACCCATACAGGGGCCCTGTACACCTTCACCTTCGGGAC</td> <td>925</td>	866 CTGTCAAGCGGGGAGAGACCCCCCAACCCATACAGGGGCCCTGTACACCTTCACCTTCGGGAC	925
Db	466 CTGTCCAGCGGTGAAGAGCCACCTCTTACAGGGGGCCCTGCACCTCTCACTCTCCGGGAC	525
QY	926 CCCGAGCAGCAGCTTGGAACTGAAACCGGGAGTTCGGTCGCGGACCCCAAGAGAACCTATC	985
Db	526 CCTGAAACCGCGAGATGGAACTCAACCGAGAGTCTCGTAGAGGGGCCCAACCCAGGAACCTA	585
QY	986 TTTCGACAGTAGCCTGATGGATAGTGGCCAGG---CTGGGGCGGGCCCTGGCCCCCGACGAGT	1042
Db	586 TTTCGACAGTAGTTTATATGACATTTCCTATGTATATAGCGGGGGTCCATGCCCCACCCAGCAGC	645
QY	1043 AACTCGGGGCATCAGCGCCACGTCGTACGCGCAGCGGGCGCGCATGAGAGGGGCCGCGGCC	1102
Db	646 AACTCGGGGCATCAGTCGCAAGCACCCTGCGAGCAGTAAACGGGAGATGGAAGGGGCCACCCCCC	705
QY	1103 AACTCAGCGCGAGGATCATCGGCACATACCCGGGGGTCCTTCCTTCAGACACAGAGAGCAG	1161
Db	706 ACATACAGCGAGGTGATGCGCCACACCCACCGCGCCTTTTCTTCCTCATACACAGGCGAG	764

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RESULT 6
US-09-103-840A-2
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

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	Query Match	5.3%	Score 70.4	DB 3:	Length 4403765
	Best Local Similarity	50.0%	Pred. No.	0.00016	
	Matches 230;	Conservative	0;	Mismatches 226;	Indels 4; Gaps 2;
OY	2	GACCGGCTTCGGAGCGAACC	CCGATCTCCTTGACTTGAATGAGAGGAGGCGC	61	
Dd	3936335	GCCGCGCGCAACGGCGGCACCGCGGCGCAGAGAGCGGCACTGGTGGCCCGCGCGCACCGT	3936394		
OY	62	GCGCGCGCGCGCGCGAGAGCGCTCGCGTGGGAAAGCTACCGCGAGAGGCTCAGCCCCG	121		
Dd	3936395	ATCGGTGGCGTGGGCGGCGGCGCAAGGCGCGCAACGGCGCGAGACGGGAGMATGGGGGTTGCG	3936455		
OY	122	GCGCGAGCGCGCGCCCGCTGCCAGACCATTTTCGGAGCGCCACCGCGGCGACTGCCG	180		
Dd	3936455	GCGCGCGCGCGCGCGAGCGGCCAACACACAGTCCC CGCGCGCAACGGCGGCGCAAGAGAAGT	3936514		
OY	181	-ACCGCCCCGGGGGCGCGAGAGGGAGTCCGGGGGGCGGCACAGGAGCGGCTCCCGCGCA	239		
Dd	3936515	CAGAGGCGCAACGGGTGTGCCGTGGGGCGGCGCGGGGCTGGCGCGCGGTGGCGGCGCT	3936574		
OY	240	CTGAGCCCGCGGCGCGCCCGGGAACATTGGCGCGCAACCGGACCGCGGCGGAGCGC	299		
Dd	3936575	AACGGCACCGGTGGCGAACAGCGGCGCAAGGCGGTGCCGCGGCACCCGAGAGGCGCGGCCCA	3936633		
OY	300	CTCTCCCCCGCGCGGCGCTCTCGATGCGAGGAGCCCACTTCGCGGCGCGGCGCGGAGCC	359		

Db	3936635	GCTCTCTCAGTATACCAACGGGGGGGGGGGGCGCCGG--CGGCAACGGAGGCGACGGCG	3936692
QY	360	CCCCCGGCGCCCCCGAGCCCCCGGCGCCCGCGCGCCCGCTCATGCAACC	419
Db	3936693	GCAACGGCGCGCGCGCGGACACCGAGGCGCGCGCACCGCGCGGGCGCGGACG	3936752
QY	420	GCATTGATGGGGTCAACAGCAGCGCGCGCGCGCGCGCGG	459
Db	3936753	GGGACCAAGTTGGCCAGAGGCGGCGCGCGCGCGGTGCCGG	3936792

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RESULT 7
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6293328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H3/rv
; US-09-103-840A-1

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Query Match	5.28: Score 68.8: DB 3: Length 4411529;
Best Local Similarity	49.88: Pred. No. 0.00033;
Matches 229; Conservative 0; Mismatches 227; Indels 4; Gaps 2;	
QY 2 GACGCGGTCTCGAGCGAACCCTGATCTCTTGACTTGATGAGGAGAGGAGCG 61	Db 3942788 GCCCGCGCAACGCGCGCACCGCGCGCAGAGCGCGCATGTGTGTGCGCGCGCGCGACGGT 3942847
QY 62 GCGCGCGCGCGCGCGCGAGCGCTCTGGCTGTGGGGGAAAGCTAAGCGCAGAGGCTCAGCCCG 121	Db 3942848 ATCTGGTGGCTGCGCGCGCGCAAGGCGGCGCAACGCGCGCGCGAGCGGCAAGTGTGCGGTGCG 3942907
QY 122 GCGGCACGCGCGCGCGCGCGTGCACGCCATTTTCGAGCGCACCGCGCGCGCACTGCGG - 180	Db 3942908 GCGCGCGCGCGCGCGCGCGACGCGGCCCAACACCACTGTCCCGCGCGCAACGCGCGCGCAAGAGGT 3942967
QY 181 -ACGCCCCCGGGGCTGCCAGGGAGCGCGGGGGGCGCACGCGAGCGGTCTCCCGCA 239	Db 3942968 CAAGCGCGCGACGCGTGTGTGCGCGGTGGGGCGCGCGCGCTGTGCGCGCGCGCGCGGT 3943027
QY 240 CTGAGCCCCCGCGCGCGCGCGCGGAACTTGTCGCGGCACCGCAACCCGCGCGAGCGCGCGCGG 299	Db 3943028 AACGGCACCGCTGGCAACGCGGGCGCCAGAGCGCGTGTCCGCGCGCACCGCGCGCGCGCGCA 3943087
QY 300 CTTTCCCCCGCGCGCGCGCTCTCTGCATCGCGGGGCCCAAGCTTCCGGGCGCGCGCGAGGCC 359	Db 3943088 GCTCTCTCTAGTTACTCAACGCGGGGAGAGCGCGCGCGCGCG -- CGGCACCGGAGGCGACGGCG 3943145
QY 360 CCCCCGCGCGCGCGCAAGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCTCATGCACC 419	Db 3943146 GCACCGCGCGCGCGCGCGCGCGCACCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3943205
QY 420 GCTTGATGGGGGTCAACGACGACGCGCGCGCGCGCGCGCG 459	Db 3943206 GCGGACAAAGTGTGCCAAGGCGCGCGCGCGCGCGCGGTGCGG 3943245

US-08-804-227C-7/c
Sequence 7, Application US/08804227C
Patent No. 5876991
GENERAL INFORMATION:
APPLICANT: Dehoff, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rostock, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804.227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35, 784
REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4437 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 350..14002
FEATURE:
NAME/KEY: CDS
LOCATION: 14046..20036
FEATURE:
NAME/KEY: CDS
LOCATION: 20110..31284
FEATURE:
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LOCATION: 31329..36071
NAME/KEY: CDS
LOCATION: 36155..41830
US-08-804-227C-7
Query Match
Best Local Similarity 5.18; Score 68; DB 2; Length 44377;
Pred. No. 0.00025;
Matches 234; Conservative 0; Mismatches 240; Indels 2; Gaps 2;
DB 5 CGCGGTCTCGAGCGAAACCCGATCTCTTGGAATGAGAGAGAGAGCGCGCGC 64
19499 CTGGGGTGGCGAAGCTCCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 19440
QY 65 GCGCGCGCGCGCGCGCGCTGCGGAAAGCTAGCGGAGAGAGCGTCACCGCGCGC 124
DB 19439 GGGGGGAGGGGCGAGCGACCGCTCTCGTCCCGGTGCGCGCGCGCGCGCGCGC 19380
QY 125 GCAGCGCGCGCGCGCGCGCTGCGACCGCATTTTTCGAGCGCGCGCGCGCGCGCGC 184
DB 19379 GCGGGCGTCCGC 19320
QY 185 CCGCGGGGCTGCGAGGGAGCGCGCGGGGGGCGCGAGCGCGCGCTCCCGCGCACTGAG 244

DB 19319 GCGCGGGGCGCGCGAGTGAAGCCGAGCGAGCGAGCGCGCGCTCGGGCCGGGT-CAAGC 19261
QY 245 CCGCGCGCGCGCGCGCGGAGCTTGGCGGCGACCGCGCGCGAGCGCGGGCGCGCGCTCC 304
DB 19260 CCGGGTCAAGCAGTGCAGTGCGGGGCGGGGTGAGAGGGGCGAGACCGCGAGCGCTGA 19201
QY 305 CCGCGCGCGCGCGCTCTCTGCAAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGC 364
DB 19200 CCGCGCGCGCGCTCTCTGCAAGTCCGCGAGAGACCGCGCGCGCGCGCGCGCGCGC 19141
QY 365 GC 424
DB 19140 AGCGAGCGAGCAGCGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 19082
QY 425 ATGGGGTGCACACAGC 480
DB 19081 AAGCGTTGGCGCGCGGTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 19026
RESULT 9
US-08-804-198-1/c
Sequence 1, Application US/08804198
Patent No. 5945320
GENERAL INFORMATION:
APPLICANT: Burgett, Stanley G.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rao, Nagaraia R.
APPLICANT: Richardson, Mark A.
APPLICANT: Rostock, Paul R., Jr.
TITLE OF INVENTION: PLATENOILIDE SYNTHASE GENE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: PAUL R. CANTRELL 1138
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804.198
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P9113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 350..14002
FEATURE:
NAME/KEY: CDS
LOCATION: 14046..20036
FEATURE:
NAME/KEY: CDS
LOCATION: 20110..31284
FEATURE:
NAME/KEY: CDS
LOCATION: 31329..36071

LENGTH: 152331
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(152331)
OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

Query Match 5.0%; Score 66; DB 3; Length 152331;
Best Local Similarity 49.1%; Pred. No. 0.0007;
Matches 189; Conservative 0; Mismatches 191; Indels 5; Gaps 1;

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QY 75 GCGGAGGCGCTCGGCTGGGGAAGCTAGCGGCGAGAGCTACGCCCGCGGCGAGCGGCG 134
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21828 GGGGTGTGACGTGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGG 21887
QY 135 CCGCGCTGCGAGCCATTTCGAGACGCGACCGCGGCGACTGCGACGCGCGCGCGGCGT 194
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    21888 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 21942
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    195 GCGGAGGCGAGCGCGGCGGCGCGAGCGGCGGTCCGCGACTGAGCGCGCGCGCG 254
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    21943 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22002
QY 255 CCGCGGGAAGCTGGGCGGCGAGCCGAGCGCGGCGAGCGCGGCGCGCGCGCGCGCG 314
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 22003 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22062
QY 315 GCTCTGTCATGCGGCGCGCGAGCTCCGCGCGCGCGAGCGCGCGCGCGCGCGCGCG 374
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    22063 CCGCGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22122
QY 375 GAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 434
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    22123 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22182
QY 435 ACAGACGCGCGCGCGCGCGCGCG 459
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    22183 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: August 27, 2003, 20:11:11
Job time : 133 secs


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OY 573 TGGTGGTGGTATCATACGTGCGCTGGTGAAGCCACTCTCAAGCTGTGTGCACGGGTCCTTCATCA 632
Db 481 TGTGTGTGTATCATCGTCTGCTGCTGTGACCACTTCACAGCTTCTGTGACGGTCTTTCATCA 540
OY 633 GCCGGCACAGCCAGGGGGGAGAGAGAGAAGATGGCTCTGTCTCTCAGAAAGATGCTGTGGC 692
Db 541 GCCGGCACAGCCAGGGGGGAGAGAGAGAAGATGGCTGTCTCTCAGAAAGATGCTGTGGC 600
OY 693 CCTGGGAGAGACAGTGTCTAGGCAACGGAATCCAGAGCCGAGGTCTACGCCGCCCTC 752
Db 601 CCTGGGAGAGACAGTGTCTAGGCAACGGAATCCAGAGCCGAGGTCTACGCCGCCCTC 660
OY 753 GGCCACACGACCGCTGGCGCTGGCGGCCCTTGGCGCCAGCGGAGGGCTTCACAGCGCTTC 812
Db 661 GGCCACACGACCGCTGGCGCTGGCGGCCCTTGGCGCCAGCGGAGGGCTTCACAGCGCTTC 720
OY 813 AGCCACACTTACCTGACCTGCAGCAGAGATCGACCTGACCCACCACTTCGTGTGTGAC 872
Db 721 AGCCACACTTACCTGACCTGCAGCAGAGATCGACCTGACCCACCACTTCGTGTGTGAC 780
OY 873 ACGGGAGAGACCCCGACCTTACCAAGGGCCCGCTGCAGCTTCAGCTTGGGACCCCGAGC 932
Db 781 ACGGGAGAGACCCCGACCTTACCAAGGGCCCGCTGCAGCTTCAGCTTGGGACCCCGAGC 840
OY 933 AGCAGCTGGAAGTGAACCGGGAGTGTGGTGGCGCACCCCGCAAAAGAAACAATCTTTCAGCA 992
Db 841 AGCAGCTGGAAGTGAACCGGGAGTGTGGTGGCGCACCCCGCAAAAGAAACAATCTTTCAGCA 900
OY 993 GTGACCTGATGATAGTATGATCCACAGGCTGGCGGGCCCGCTGGCCCGCCAGCAGTAACTGGGCA 1052
Db 901 GTGACCTGATGATAGTATGATCCACAGGCTGGCGGGCCCGCTGGCCCGCCAGCAGTAACTGGGCA 960
OY 1053 TCAGGGCCACGTGCTACGGCAGCGGGCGGCGCATGTGAGGGGCGCGCCCACTTACAGCG 1112
Db 961 TCAGGGCCACGTGCTACGGCAGCGGGCGGCGCATGTGAGGGGCGCGCCCACTTACAGCG 1020
OY 1113 AGGTCAATGGGCGACACTACCCGGGGTTCCTCTTCACAGCACACAGCAGTGTGGGCGGCCCT 1172
Db 1021 AGGTCAATGGGCGACACTACCCGGGGTTCCTCTTCACAGCACACAGCAGTGTGGGCGGCCCT 1080
OY 1173 CTTTGTGTGAGGGGAGCCCGGCTCCACACACACATATGCGCCCTTAGAGAGCGCAGCA 1232
Db 1081 CTTTGTGTGAGGGGAGCCCGGCTCCACACACACATATGCGCCCTTAGAGAGCGCAGCA 1140
OY 1233 TCTGGAGCAAGAAGATTAACAAGAAAGACACCTCTTAGGGTCCCGAGGGGGGCC 1292
Db 1141 TCTGGAGCAAGAAGATTAACAAGAAAGACACCTCTTAGGGTCCCGAGGGGGGCC 1200
OY 1293 GGCGTGGGGCTGCGTAGGTGAAGAAAGCAG 1321
Db 1201 GGCGTGGGGCTGCGTAGGTGAAGAAAGCAG 1229

RESULT 3
US-09-934-249-3
; Sequence 3, Application US/09934249
; Patent No. US20020115081A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Richard T.
; APPLICANT: Landschulz, Katherine T.
; APPLICANT: Turi, Thomas G.
; APPLICANT: Thompson, John F.
; APPLICANT: Kennedy, Scott P.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
; FILE REFERENCE: P0738/77001/ERP/EA
; CURRENT APPLICATION NUMBER: US/09/934,249
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/227,159
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 3
; LENGTH: 861
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(861)
US-09-934-249-3

Query Match      65.2%; Score 861; DB 10; Length 861;
Best Local Similarity 100.0%; Pred.No.1.ee-180;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY    413 ATGCACCGCTGATGGGGGTCAACAGCACCACGCCGCCGCCGCCGCCGCCAGCCCAATGTC 472
Db     1 ATGCACCGCTGATGGGGGTCAACAGCACCCGCCGCCGCCGCCGCCGCCAATGTC   60

OY    473 TCCTGCACGTGCACAACCTGCAAACGCTCTTTGTTCCAGAACATGAGATCAGGACTGGAG 532
Db     61 TCCTGCACGTGCACAACCTGCAAACGCTCTTTGTTCCAGAACATGAGATCAGGACTGGAG 120

OY    533 TTTGTCGATCATCATCATCATGTCGTGGTGGTGAATGATGGATGGTGATGATCATACGTGC 592
Db    121 TTTGTCGATCATCATCATCATGTCGTGGTGGTGAATGATGGATGGTGATGATCATACGTGC 180

OY    593 CTGCTGACCCACTACAAAGCTGTCTGCACAGTCCTCTTCATCAGCCCGGACAGCAGGGCGG 652
Db    181 CTGCTGACCCACTACAAAGCTGTCTGCACAGTCCTCTTCATCAGCCCGGACAGCAGGGCGG 240

OY    653 AGGAGAGAAGATGCCCTGTCTCTCAGAAAGATGCTGTGGCCCCCTGGAGAGACAGTGTCA 712
Db    241 AGGAGAGAAGATGCCCTGTCTCTCAGAAAGATGCTGTGGCCCCCTGGAGAGACAGTGTCA 300

OY    713 GGCAACGGAATCCCCAGAGCCCGAGGTATAGCCGCCGCCGCCGCCGCCACGACGCGCTGGCC 772
Db    301 GGCAACGGAATCCCCAGAGCCCGAGGTATAGCCGCCGCCGCCGCCGCCACGACGCGCTGGCC 360

OY    773 GTGCCGCCCTTGCGCCACAGGGGAGCGCTTCACACGCTTCCAGCCACCATTACGTACTGT 832
Db    361 GTGCCGCCCTTGCGCCACAGGGGAGCGCTTCACACGCTTCCAGCCACCATTACGTACTGT 420

OY    833 CAGCAGCAGATATGACATCTGGCCAACCAATCTTCGTGTAGACGGGGAGAGACCCCCACCC 892
Db    421 CAGCAGCAGATATGACATCTGGCCAACCAATCTTCGTGTAGACGGGGAGAGACCCCCACCC 480

OY    893 TACCAAGGCCCCCTGACACCTTCACAGTTTCGGGACCCCGAGCAGAGCTGGAATTAACGG 952
Db    481 TACCAAGGCCCCCTGACACCTTCACAGTTTCGGGACCCCGAGCAGAGCTGGAATTAACGG 540

OY    953 GAGTCGTGTGGCGGCACACCCCAAAGAACCAATCTTCGACAGTAGCTATGATAGTGTCC 1012
Db    541 GAGTCGTGTGGCGGCACACCCCAAAGAACCAATCTTCGACAGTAGCTATGATAGTGTCC 600

OY    1013 AGGCTGGGCGGCGCCCTTGCCGCCCGCCAGCAGTAACTCGGGGCAATCAGAGGCCACGTGACGGC 1072Z
Db    601 AGGCTGGGCGGCGCCCTTGCCGCCCGCCAGCAGTAACTCGGGGCAATCAGAGGCCACGTGACGGC 660

OY    1073 AGCGGCGGGGCGATGAGAGGGGCGCGCGCCACACTTACAGCGAGGTATCGGCGACTACCGG 1132Z
Db    661 AGCGGCGGGGCGATGAGAGGGGCGCGCGCCCGCCCACTTACAGCGAGGTATCGGCGACTACCGG 720

OY    1133 GGGTCTCTCTTCCAGACACAGCAGAGAGTGGGGCGCCCTCTCTGTGTAGAGGAGACCCGG 1192Z
Db    721 GGGTCTCTCTTCCAGACACAGCAGAGAGTGGGGCGCCCTCTCTGTGTAGAGGAGACCCGG 780

OY    1193 CTCACACACACACATCGCGCCCTTAGAGAGCCAGCCATCTGGAGCAAGAGAAAGAT 1252Z
Db    781 CTCACACACACACATCGCGCCCTTAGAGAGCCAGCCATCTGGAGCAAGAGAAAGAT 840

OY    1253 AAACAGAAAGACACCTCTC 1273
Db    841 AAACAGAAAGACACCTCTC 861

```

RESULT 4
 US-09-796-753-55
 ; Sequence 55, Application US/09796753
 ; Publication No. US20030027998A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McCarthy, Sean A.
 ; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
 ; FILE REFERENCE: 7853-227-999
 ; CURRENT APPLICATION NUMBER: US/09/796,753
 ; CURRENT FILING DATE: 2001-03-01
 ; PRIOR APPLICATION NUMBER: 09/183,175
 ; PRIOR FILING DATE: 1998-10-30
 ; PRIOR APPLICATION NUMBER: 09/223,094
 ; PRIOR FILING DATE: 1998-12-30
 ; PRIOR APPLICATION NUMBER: 09/223,546
 ; PRIOR FILING DATE: 1998-12-30
 ; PRIOR APPLICATION NUMBER: 09/224,246
 ; PRIOR FILING DATE: 1998-12-30
 ; PRIOR APPLICATION NUMBER: 09/259,388
 ; PRIOR FILING DATE: 1999-02-26
 ; PRIOR APPLICATION NUMBER: 60/122,458
 ; PRIOR FILING DATE: 1999-03-01
 ; PRIOR APPLICATION NUMBER: 09/312,359
 ; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: 09/336,536
 ; PRIOR FILING DATE: 1999-06-18
 ; PRIOR APPLICATION NUMBER: 09/342,687
 ; PRIOR FILING DATE: 1999-06-29
 ; PRIOR APPLICATION NUMBER: 09/345,464
 ; PRIOR FILING DATE: 1999-06-30
 ; PRIOR APPLICATION NUMBER: 09/365,164
 ; PRIOR FILING DATE: 1999-07-30
 ; PRIOR APPLICATION NUMBER: 09/399,723
 ; PRIOR FILING DATE: 1999-09-20
 ; PRIOR APPLICATION NUMBER: 09/409,634
 ; PRIOR FILING DATE: 1999-09-30
 ; PRIOR APPLICATION NUMBER: 09/471,179
 ; PRIOR FILING DATE: 1999-12-23
 ; PRIOR APPLICATION NUMBER: 09/474,071
 ; PRIOR FILING DATE: 1999-12-29
 ; PRIOR APPLICATION NUMBER: 09/474,072
 ; PRIOR FILING DATE: 1999-12-29
 ; PRIOR APPLICATION NUMBER: 09/514,010
 ; PRIOR FILING DATE: 2000-02-25
 ; PRIOR APPLICATION NUMBER: 09/516,745
 ; PRIOR FILING DATE: 2000-03-01
 ; PRIOR APPLICATION NUMBER: 09/572,002
 ; PRIOR FILING DATE: 2000-05-14
 ; PRIOR APPLICATION NUMBER: 09/597,993
 ; PRIOR FILING DATE: 2000-06-19
 ; PRIOR APPLICATION NUMBER: 09/599,596
 ; PRIOR FILING DATE: 2000-06-22
 ; PRIOR APPLICATION NUMBER: 09/630,334
 ; PRIOR FILING DATE: 2000-07-31
 ; PRIOR APPLICATION NUMBER: 09/606,565
 ; PRIOR FILING DATE: 2000-06-29
 ; PRIOR APPLICATION NUMBER: 09/606,317
 ; PRIOR FILING DATE: 2000-06-29
 ; PRIOR APPLICATION NUMBER: 09/665,666
 ; PRIOR FILING DATE: 2000-09-20
 ; PRIOR APPLICATION NUMBER: 09/677,751
 ; PRIOR FILING DATE: 2000-09-30
 ; NUMBER OF SEQ ID NOS: 162
 ; SEQ ID NO 55
 ; LENGTH: 969
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (6)...(761)
 ; US-09-796-753-55

Query Match 60.8%; Score 803.2; DB 11; Length 969;
 Best Local Similarity 99.6%; Pred. No. 8.4e-168;
 Matches 805; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	514	GGAGATCAGGAGCTGGAGATTGTTCAATCATCATCTGCTGGTGTATATATGTTAT	573
DB	2	GGAGATGGGGAGGAGCTGGAGATTGTTCAATCATCATCTGCTGGTGTATATGTTAT	61
QY	574	GGTGGTGTATCATACGCTGCTGCTGAGCAGTACAGAGCTGTGACAGGGTCTTATCAG	633
DB	62	GGTGGTGTATCATACGCTGCTGCTGAGCAGTACAGAGCTGTGACAGGGTCTTATCAG	121
QY	634	CCGGACACAGCCAGGGGGGAGAGAGAGATGCTGCTTCAAGAGATGCTTGGCC	693
DB	122	CCGGACACAGCCAGGGGGGAGAGAGAGATGCTGCTTCAAGAGATGCTTGGCC	181
QY	694	CTCGAGAGACAGATGTACAGCAAGCAATCCAGAGCCGAGAGTCTAGCCCGCTCG	753
DB	182	CTCGAGAGACAGATGTACAGCAAGCAATCCAGAGCCGAGAGTCTAGCCCGCTCG	241
QY	754	GCCACCCAGCCGCTGGCGCTGCGCCCTTCCGCCAGCGGAGCGCTTCCAGCGTTCCA	813
DB	242	GCCACCCAGCCGCTGGCGCTGCGCCCTTCCGCCAGCGGAGCGCTTCCAGCGTTCCA	301
QY	814	GCCACCTATTCGCTACCTGACAGCAGATGCACTGCCACCCACCATCTGCTGTACA	873
DB	302	GCCACCTATTCGCTACCTGACAGCAGATGCACTGCCACCCACCATCTGCTGTACA	361
QY	874	CGGGAGAGAGCCGCCACCTTACAGGGGCCCTTCCAGCTTCCAGAGCCCGAGCA	933
DB	362	CGGGAGAGAGCCGCCACCTTACAGGGGCCCTTCCAGCTTCCAGAGCCCGAGCA	421
QY	934	GCAGCTGGAATGAACCGGAGTGGTGGCGGACCCCAACAGAACCATCTTGCAGCAG	993
DB	422	GCAGCTGGAATGAACCGGAGTGGTGGCGGACCCCAACAGAACCATCTTGCAGCAG	481
QY	994	TGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1053
DB	482	TGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	541
QY	1054	CAGCGCCAGCTGTACAGGAGCGGGGGGAGTGAAGGGGGGCGCCGCCACCTTACAGCA	1113
DB	542	CAGCGCCAGCTGTGTACAGGAGCGGGGGGAGTGAAGGGGGGCGCCGCCACCTTACAGCA	601
QY	1114	GCTATCGGCGCTACCTCGGGGCTCTCTTCCAGACACAGCAGAGCAGTGGGCCCTTC	1173
DB	602	GCTATCGGCGCTACCTCGGGGCTCTCTTCCAGACACAGCAGAGCAGTGGGCCCTTC	661
QY	1174	CTTGCTGGAGGGAGCCGGGCTCCACACACACATCGGGGCCCTTGAAGAGGGACGCAT	1233
DB	662	CTTGCTGGAGGGAGCCGGGCTCCACACACACATCGGGGCCCTTGAAGAGGGACGCAT	721
QY	1234	CTGGACCAAGAGAGAGATTAACAGAAAGACACCTCTCTAGAGTCCCGAGGGGGCGG	1293
DB	722	CTGGACCAAGAGAGAGATTAACAGAAAGACACCTCTCTAGAGTCCCGAGGGGGCGG	781
QY	1294	GGCTGGGGCTGCTAGGTGAAAAGCAG 1321	
DB	782	GGCTGGGGCTGCTAGGTGAAAAGCAG 809	

RESULT 5
 US-10-301-822-208
 ; Sequence 208, Application US/10301822
 ; Publication No. US20030148410A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Berger, Allison
 ; APPLICANT: Guillemette, Tracy L.
 ; APPLICANT: Kamatkar, Shubhangi
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Monahan, John E.
 ; APPLICANT: Thibodeau, Stephen N.

Db 317 CTAGGCCCCGCTCTGGGCCACGACGCGCTGGCGCTGCGCCCTTGCGCCAGGGAGCG 376

QY 799 CTTCACACGCTTCCAGCCACCTATCCGTACTGTACGTACGACGACGAGATGAGCTCGCAC 858

Db 377 CTTCACACGCTTCCAGCCACCTATCCGTACTGTACGTACGACGAGATGAGCTCGCAC 436

QY 859 CATCTGCGTGTCCAGAGGGGGAGAGAGCCCACTTACAGAGGGCCCTGCACTCCAGCT 918

Db 437 CATCTGCGTGTCCAGAGGGGGAGAGAGCCCACTTACAGAGGGCCCTGCACTCCAGCT 496

QY 919 TCGGGACCCCGAGCAGCAGCTGGAATGAACCGGGAGTGGTGGCGGCACCCCAACAG 978

Db 497 TCGGGACCCCGAGCAGCAGCTGGAATGAACCGGGAGTGGTGGCGGCACCCCAACAG 556

QY 979 AACCATCTTCGACAGTGAACCTATGATATGTCCAGAGGCTGGGGCCCTGCCCCCAG 1031

Db 557 AACCATCTTCGACAGTGAACCTATGATATGTCCAGAGGCTGGGGCCCTGCCCCCAG 616

1039 CAGTACTCGGGCATCAGCGGCACCTGTGTACGGCGAGCGGGGGCCATGAGAGGGCGCC 1098

617 CAGTAACTCGGGCATCAGCGGCACCTGTGTACGGCGAGCGGGGGCCATGAGAGGGCGCC 676

1099 GCCCACCCTACAGCGAGGTCAATGGCCACTACCCGGGGTCTCTCTTCACGACACGACAG 1158

Db 677 GCCCACCCTACAGCGAGGTCAATGGCCACTACCCGGGGTCTCTCTTCACGACACGACAG 736

QY 1159 CAGTGGGCGCCCTCTCTGTGTGAGAGGAGACCGGGCTCCACACACACATCGCGCCCT 1218

Db 737 CAGTGGGCGCCCTCTCTGTGTGAGAGGAGACCGGGCTCCACACACACATCGCGCCCT 796

QY 1219 AGAGAGGCGAGCCATCTGGAGCAAAAGAAAGATAAACAGAAAGACACCTCTCTAGG 1278

Db 797 AGAGAGGCGAGCCATCTGGAGCAAAAGAAAGATAAACAGAAAGACACCTCTCTAGG 856

QY 1279 TCCCCAGAGGGGCGCGGCTGGGGCTGGGTAGGTAAAGGCGAG 1331

Db 857 TCCCCAGAGGGGCGCGGCTGGGGCTGGGTAGGTAAAGGCGAG 899

US-10-241-220-44
RESULT 7
Sequence 44, Application US/10241220
Publication No. US20030148408A1
GENERAL INFORMATION:
APPLICANT: Franz, Gretchen
APPLICANT: Hillan, Kenneth J.
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
APPLICANT: Spencer, Susan
APPLICANT: Williams, P. Mickey
APPLICANT: Wu, Thomas
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF TUMOR
FILE REFERENCE: P5010R1-US
CURRENT APPLICATION NUMBER: US/10/241,220
CURRENT FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 44
LENGTH: 1850
TYPE: DNA
ORGANISM: Homo Sapien
US-10-241-220-44

Query Match	60.7%	Score 802.2	DB 12	Length 1850
Best Local Similarity	98.4%	Ped NO. 14e157		
Matches 810	Conservative	0	Mismatches 13	Indels 0
				Gaps 0
QY	499	TTTGTGCCGAGCATGAGATCAGGACGCGCGATTTGTCACATCATCATCTGTGT	558	
Db	77	TCTCCGGAACACGAGCATGTGGGAGCTGGATTGTTCACATCATCATCATGTGT	136	

QY	559	GCGATGATGTGATGTGGTGGTGATCATCAGTCCTGCCTGAGACCACTCAAGCTGTGC	611
Db	137	GGGATGATGATGTGATGTGGTGGTGATCATCAGTCCTGCCTGAGACCACTCAAGCTGTGC	198
QY	619	ACGGTCCTTCATCAGCGCCGACACAGGCCGGGGAGAGAAAGATGCCCCGTCTCAGA	675
Db	197	ACGGTCCTTCATCAGCGCCGACACAGGCCGGGGAGAGAAAGATGCCCCGTCTCAGA	255
QY	679	AGGATGCTGTGCGCCCTCGAGAGACAGTGTCAAGGCAAGGAAATCCCAGATCGGCAAGT	735
Db	257	AGGATGCTGTGCGCCCTCGAGAGACAGTGTCAAGGCAAGGAAATCCCAGATCGGCAAGT	318
QY	739	CTACGCCCCGCGCTCGGCCACCAGAACCGCTGGCCGTGCGCCCTTCGCCACAGGGAGCG	798
Db	317	CTACGCCCCGCGCTCGGCCACCAGAACCGCTGGCCGTGCGCCCTTCGCCACAGGGAGCG	376
QY	799	CTTCCACCGCTTCCACGCCCACTTAACGTACTCTCACAGAGATCAACCTGGCACCCAC	858
Db	377	CTTCCACCGCTTCCACGCCCACTTAACGTACTCTCACAGAGATCAACCTGGCACCCAC	436
QY	859	CATCTCGCTGTACAACGGGAGAGAGCCCAACCCCTACCAAGGCCCTGTGCACCTCCAGCT	918
Db	437	CATCTCGCTGTACAACGGGAGAGAGCCCAACCCCTACCAAGGCCCTGTGCACCTCCAGCT	496
QY	919	TCCGGACCCCGAGAGAGAGCTGGAACTGAACCGGGAGTCTGGTCGCGCAACCCCAAACAG	978
Db	497	TCCGGACCCCGAGAGAGAGCTGGAACTGAACCGGGAGTCTGGTCGCGCAACCCCAAACAG	556
QY	979	AACCATTTGACAGATGACTGTAGTAGTGCAGAGCTGGGGGGGGCCCTGGCCCCCGCCAG	1033
Db	557	AACCATTTGACAGATGACTGTAGTAGTGCAGAGCTGGGGGGGGCCCTGGCCCCCGCCAG	616
QY	1039	CAGTAACTCGGGGATAGAGGCCACAGCTGAACGCGACGGCGGGCGCATGAGAGGGCGGC	1098
Db	617	CAGTAACTCGGGGATAGAGGCCACAGCTGAACGCGACGGCGGGCGCATGAGAGGGCGGC	676
QY	1099	GCCCCACTTACAGGAGGTATGGCCACTACACCCGGGGTCTCTCTTCACGACNCACACAAAG	1158
Db	677	GCCCCACTTACAGGAGGTATGGCCACTACACCCGGGGTCTCTCTTCACGACNCACACAAAG	736
QY	1159	CAGTGGCGCGCCCTCTTCTGTAAGGGAGCCCGCTCCACACACACATCGGCCCT	1218
Db	737	CAGTGGCGCGCCCTCTTCTGTAAGGGAGCCCGCTCCACACACACATCGGCCCT	796
QY	1219	AAGAGCGCAGCCATCTGTGAGCAAAAGAGAAAGATTAACAGAAAGACACCTCTTAAGG	1278
Db	797	AAGAGCGCAGCCATCTGTGAGCAAAAGAGAAAGATTAACAGAAAGACACCTCTTAAGG	856
QY	1279	TCCCAGAGGGGGCGGGCTGGGGGCTGCGCTAAGTGA AAAAGCAG 1321	
Db	857	TCCCAGAGGGGGCGGGCTGGGGGCTGCGCTAAGTGA AAAAGCAG 899	

```

RESULT 8
US-10-098-841-71
: Sequence 71, APPENDICATION US/10098841
: Publication NO. US20020197679A1
: GENERAL INFORMATION:
:
: APPLICANT: Tang, Y. Tom
: APPLICANT: Liu, Chenghua
: APPLICANT: Asundi, Vinod
: APPLICANT: Xu, Chongjun
: APPLICANT: Zhou, Ping
: APPLICANT: Ma, Yundong
: APPLICANT: Wang, Jian-Rui
: APPLICANT: Zhao, Qing A.
: APPLICANT: Ren, Feiyen
: APPLICANT: Chen, Ruihong
: APPLICANT: Wang, Duntui
: APPLICANT: Wang, Zhiwei
: APPLICANT: Weinman, Tom
: APPLICANT: Zhang, Jie
: APPLICANT: Qian, Xiaohong B.

```


Db 825 GCGCCGAGGCTCTACGCCCCGCTCGGCCACGACGCGCTGGCCGCTTCCGCC 884
Qy 788 CAGCGGAGAGCGCTTCCAGCGCTTCCAGCGCACTTATCCGCTACGACAGAGATGAC 847
Db 885 CAGCGGAGAGCGCTTCCAGCGCTTCCAGCGCACTTATCCGCTACGACAGAGATGAC 944
Qy 848 CTGCGACCGACATCTGCTGTGACAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 907
Db 945 CTGCGACCGACATCTGCTGTGACAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1004
Qy 908 ACCGTCGAGCTTGGGAG 967
Db 1005 ACCGTCGAGCTTGGGAG 1064
Qy 968 CCCCCAAG 1027
Db 1065 CCCCCAAG 1124
Qy 1028 TGCCCCCGACAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1087
Db 1125 TGCCCCCGACAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1184
Qy 1088 GAGGGGGGCG 1147
Db 1185 GAGGGGGGCG 1244
Qy 1148 CACGAG 1207
Db 1245 CACGAG 1304
Qy 1208 ATCG 1267
Db 1305 ATCG 1364
Qy 1268 CCTCTCTAGGGTCCCGAGGGGGGCGGGGCTGGGTGGGTGGGTGGGTGGGTGGGTGG 1321
Db 1365 CCTCTCTAGGGTCCCGAGGGGGGCGGGGCTGGGTGGGTGGGTGGGTGGGTGGGTGG 1418

RESULT 12

US-09-934-249-14/c
; Sequence 14, Application US/09934249
; Patent No. US20020115081A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Richard T.
; APPLICANT: Landshulz, Katherine T.
; APPLICANT: Turi, Thomas G.
; APPLICANT: Thompson, John F.
; APPLICANT: Kennedy, Scott P.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: P0738/7001/ERP/KA
; CURRENT APPLICATION NUMBER: US/09/934,249
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/227,159
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (639)..
; OTHER INFORMATION: a, c, g, or t/u
US-09-934-249-14

Query Match 37.4%; Score 493.6; DB 10; Length 693;
Best Local Similarity 97.4%; Pred. No. 1.2e-99;
Matches 533; Conservative 0; Mismatches 10; Indels 4; Gaps 3;

Qy 776 CCGCCCTTGGCCAGCGGAGCGCTTCCACGCGTTCCAGCCGCACTATCCGATCTGACG 835

Db 693 CCGCCCTTGGCCAGCGGAGCGCTTCCACGCGTTCCAGCCGCACTATCCGATCTGACG 634
Qy 836 CACGAGATGAG 895
Db 633 CACGAGATGAG 577
Qy 896 CAGGAG 955
Db 576 CAGGAG 517
Qy 936 TCGGTGCGGAG 1015
Db 516 TCGGTGCGGAG 457
Qy 1016 CCGGGGGGCG 1075
Db 456 CCGGGGGGCG 397
Qy 1076 GCGGGGCGAG 1135
Db 396 GCGGGGCGAG 337
Qy 1136 TCGTCTTCCAG 1194
Db 336 TCGTCTTCCAG 277
Qy 1195 CCACGAG 1254
Db 276 CCGGAG 217
Qy 1255 ACAGAAAG 1314
Db 216 ACAGAAAG 157
Qy 1315 AAGGCGAG 1321
Db 156 AAGGCGAG 150

RESULT 13

US-09-796-753-57
; Sequence 57, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723

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PRIORITY FILING DATE: 1999-09-20
PRIORITY APPLICATION NUMBER: 09/409,634
PRIORITY FILING DATE: 1999-09-30
PRIORITY APPLICATION NUMBER: 09/471,179
PRIORITY FILING DATE: 1999-12-23
PRIORITY APPLICATION NUMBER: 09/474,071
PRIORITY FILING DATE: 1999-12-29
PRIORITY APPLICATION NUMBER: 09/474,072
PRIORITY FILING DATE: 1999-12-29
PRIORITY APPLICATION NUMBER: 09/514,010
PRIORITY FILING DATE: 2000-02-25
PRIORITY APPLICATION NUMBER: 09/516,745
PRIORITY FILING DATE: 2000-03-01
PRIORITY APPLICATION NUMBER: 09/572,002
PRIORITY FILING DATE: 2000-05-14
PRIORITY APPLICATION NUMBER: 09/597,993
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PRIORITY APPLICATION NUMBER: 09/606,565
PRIORITY FILING DATE: 2000-06-29
PRIORITY APPLICATION NUMBER: 09/606,317
PRIORITY FILING DATE: 2000-06-29
PRIORITY APPLICATION NUMBER: 09/665,666
PRIORITY FILING DATE: 2000-09-20
PRIORITY APPLICATION NUMBER: 09/677,751
PRIORITY FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 57
LENGTH: 1713
TYPE: DNA
ORGANISM: Mouse
FEATURE:
NAME/KEY: CDS
LOCATION: (2)...(652)
US-09-796-753-57

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Query Match 35.3%; Score 466.2; DB 11; Length 1713;
Best Local Similarity 83.9%; Pred. No. 1.3e-93;
Matches 573; Conservative 0; Mismatches 83; Indels 27; Gaps 3;

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QY 595 GCTGAGCCACTACAGAGTGTCTGACAGGTCCTTCATACGCCGACACAGGCGGAG 654
DB 1 GCTGAGCCACTACAGAGTGTCTGACAGGTCCTTCATACGCCGACACAGGCGGAG 60
QY 655 GAGAGAGATGCCCTGTCTCTCAGAGAGATGCTGTGGCCCTCGAGAGACAGTGTGAGG 714
DB 61 GAGAGAGATGAGTGTCTCTCAGAGAGATGCTGTGGCCCTCGAGAGAGTGTGAGG 120
QY 715 CAACGGAATCCGAGAGCGGAGGTCTACGCCCGGCTCGGCCACCGAGCGCTGGCGGT 774
DB 121 ---TGAATCCGAGAGCGGAGGTCTATGCCCGCTCGGCCACAGAGCGAGTGTGAGG 177
QY 775 GCCGCTTCGCGAGGAGGAGGCTTCCAGCGCTTCAGGCCCGACCTATCCGACTGCA 834
DB 178 GCCGCTTCATCAGAGG-----AGCGATTCACACCGACTACCGCTTACCTGCA 228
QY 835 GCACGAGATGACCTGCGACCCACCATCTGCTGTGAGAGGAGGAGGAGCGCCACCTTA 894
DB 229 GCACGAAATGCGCTGCGACCCACCATCTGCTGTGAGAGGAGGAGGAGCGCCACCTTA 288
QY 895 CCAGGCGCCCTGACCTTCAGCTTGGGAGCGCGAGCAGAGCTGAACTGAACCGGGA 954
DB 289 CCAGGCGCCCTGACCTTCAGCTTGGGAGCGCGAGCAGAGCTGAACTGAACCGGGA 348
QY 955 GTCTGTCGCGACCGCCAAACAGACATCTTGCAGAGTGAACCTGAGTGAATGAGCCAG 1014
DB 349 ATGTGTGCGCGACCGCCCTTACCGAGCATCTTTCGACAGTGAACCTTATGAGACAGCAT 408
QY 1015 GCTGGGCGCGCCCTTGCCTCCAGCATGTAATCGGGCATCAGCGCACGTGTACGGGAG 1074

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DB 409 GCTGGGGGCGCCCTGTCCCGCCAGACAGTACCTCGGCGCATCAGCCGACCTGTACAGCAG 468
QY 1075 CGCGGGCGCATGAGGAGGCGCGCCGACCTACAGAGAGTGTATCGCCGACCTACCGGAG 1134
DB 469 CGGTGGCGCATGAGGAGGCGCGCCGACCTACAGAGAGTGTATGCGACATACCTGCG 528
QY 1135 GTCTGCTTCAGAGACAGACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1194
DB 529 CTCTGCTTCAGAGACAGACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 588
QY 1195 CCACACACACATTCGCGCGCCCTAGAGAGCGGACCATGTGAGAGCAAGAGAGATTA 1254
DB 589 CCATCACTCGACATGCGCCGACCTGGA-----GACACAGAGAGAGAGAG 633
QY 1255 ACAGAAAGGACACCTCTTACAG 1277
DB 634 ACAGAAAGGATCACCCTTACAG 656

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RESULT 14
US-09-934-249-16
Sequence 16, Application US/09934249
Patent No. US20020115081A1
GENERAL INFORMATION:
APPLICANT: Lee, Richard T.
APPLICANT: Landschultz, Katherine T.
APPLICANT: Turti, Thomas G.
APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
FILE REFERENCE: P0738/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934,249
PRIORITY FILING DATE: 2001-08-21
PRIORITY APPLICATION NUMBER: US 60/227,159
PRIORITY FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 8093
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (6477)...(6477)
OTHER INFORMATION: c or t/u
NAME/KEY: unsure
LOCATION: (6837)...(6837)
OTHER INFORMATION: a or c
US-09-934-249-16

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Query Match 26.4%; Score 349; DB 10; Length 8093;
Best Local Similarity 73.7%; Pred. No. 7.9e-68;
Matches 474; Conservative 0; Mismatches 160; Indels 9; Gaps 2;

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DB 250 CGAGCTGAGATTGTTCATCATCATCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 309
QY 582 TGATACGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 641
DB 310 TGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 369
QY 642 GCCAGGGCGGAGAGAGAGATGCGCTGCTGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGT 701
DB 370 ACCAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 429
QY 702 GCACAGTGTACAGGAAATCCAGAGCGGAGGTGTACGCGCGCGCGCGCGCGCGCGCGCGCG 761
DB 430 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 483
QY 762 ACCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 821

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Db	544	ACCCCTATGTGCAGCAGCAGATTGATCTTCTCCACCACCATCTCCCTGTGCCAGGGTGAAG	603
OY	882	AGCCCCACCCCTACGAGGGGCCCCGCAACCCCTCCAGCCTTCGGGAGCCCCCAGCAGCGCTGG	941
Db	604	AGCCACCTCTCTTACCGAGGGGCCCCCTGCACCTCTGCACGCTCCGGGACCTTACACGACGATGG	663
OY	942	AACCTGAACCGGGAGTGGGTGCGCGCACCCCCAAAAGAGAACCATCTTCGACAGTGACTGA	1001
Db	664	AACCTCAACCGAGAGATCTCCTGAGGGGCCCAACCCAAACCGAACAATATTTCACAGTGAATTTAA	723
OY	1002	TGGATAGTGCCAGG---CTGGGGCGGCCCCCTGCCCCCCCAGCAGATTACTCGGGCATCAGCG	1056
Db	724	TAGCATTGTCTATGTATGATAGCGGGGGTCCATGCCCCCAGCAGGACAACTCGGGCATCACTG	783
OY	1059	CCAGGTGTTACGGGACGCGCGGGGGCGCATGAGAGGGGCCCCCGCCCATCAGACGAGGTCA	1116
Db	784	CAACACACTTGAGCAGATTAACGGGAGGAGTGGAGGGGCCACCCCCCAATATCAAGCGAGGTGA	843
OY	1119	TCGGCCACTACCGGGGCTCTCTCTTCCAGCAGCAGCAGAGCAG	1161
Db	844	TGGGCGCACACCCAGGCGCTCTTTTCTTCACATCAGCAGCGCAG	886

RESULT 15
 US-09-934-249-15
 Sequence 15, Application US/09934249
 Patent No. US20020115081A1
 GENERAL INFORMATION:
 APPLICANT: Lee, Richard T.
 APPLICANT: Landschulz, Katherine T.
 APPLICANT: Turi, Thomas G.
 APPLICANT: Thompson, John F.
 APPLICANT: Kennedy, Scott P.
 TITLE OF INVENTION: DIGNOSIS AND TREATMENT OF
 TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
 FILE REFERENCE: P0798/7001/ERP/KA
 CURRENT APPLICATION NUMBER: US/09/934,249
 CURRENT FILING DATE: 2001-08-21
 PRIOR APPLICATION NUMBER: US 60/227,159
 PRIOR FILING DATE: 2000-08-22
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 15
 LENGTH: 475
 TYPE: DNA
 ORGANISM: Mus Musculus
 US-09-934-249-15

Query Match	25.9%	Score 341.8	DB 10	Length 475
Best Local Similarity	85.5%	Pred. No. 3e-66		
Matches 408; Conservative	0	Mismatches 57	Indels 12	Gaps 2

[illegible]

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 Db 310 --TGGATGCGGAGGACACAGGTCTATGCGCCCGCTCGGACCATGACCGCATGGCGTGTG 3670
 Oy 776 CCGCCCTTGCGCCAGCGGGAGCGCTTCACCGCTTCACGCCACCTATCCGTACTCTGAG 8350
 Db 368 CCGCCCTTATCCAGGG-----AGCGATTCCACCCACCTTACCTTACTCTGAG 4180
 Oy 836 CAGAGATGCACTTGCACACCAACATCTTGCTGACAGGGGAGAGACCCCAACC 8920
 Db 419 CAGAGATTTCCTTGCACACCAACATCTTACTGTGTGATGGGAGAGACCCCAACC 4750

Search completed: August 27, 2003, 21:35:09
Job time : 390 secs

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